

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 5, 2005, 17:43:36 ; Search time 43 Seconds  
(without alignments)  
430.534 Million cell updates/sec

Title: US-10-006-856A-194  
Perfect score: 1374  
Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVITYICKYVDWIRMNRN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
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5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1359.5	98.9	249	4	US-09-949-016-8151
2	1301	94.7	254	4	US-09-949-016-6948
3	811	59.0	162	4	US-09-244-111-6
4	630.5	45.9	260	4	US-09-618-259-7
5	626.5	45.6	260	3	US-09-070-526-2
6	622.5	45.3	260	3	US-09-025-059-3
7	622.5	45.3	260	3	US-09-008-271A-7
8	622.5	45.3	260	4	US-09-618-259-8
9	618.5	45.0	250	4	US-09-205-258-427
10	618.5	45.0	282	3	US-09-025-059-1
11	602.5	43.9	288	4	US-09-386-642-13
12	598.5	43.6	289	4	US-09-386-642-14
13	597.5	43.5	248	3	US-08-944-483-24
14	573	41.7	247	2	US-08-956-267A-2
15	567	41.3	290	4	US-09-949-016-8166
16	564.5	41.1	270	4	US-09-949-016-7712
17	564.5	41.1	293	4	US-09-509-908-2
18	564	41.0	276	1	US-08-467-155A-1
19	564	41.0	276	2	US-08-628-198-1
20	564	41.0	276	3	US-09-201-038-1
21	564	41.0	276	5	PCT-US96-07343-1
22	563	41.0	325	4	US-09-949-016-7713
23	561	40.8	244	1	US-08-361-395-1
24	555	40.4	253	2	US-08-557-146-2
25	555	40.4	253	2	US-08-824-874-3
26	555	40.4	253	2	US-09-154-344-2
27	555	40.4	253	3	US-08-930-188-2

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29	555	40.4	253	4	US-09-764-762-3	Sequence 3, Appli
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31	555	40.4	265	4	US-09-949-016-7716	Sequence 7716, Ap
32	552	40.2	229	3	US-09-120-582-2	Sequence 2, Appli
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34	547	39.8	223	1	US-08-483-859-9	Sequence 9, Appli
35	547	39.8	223	1	US-08-472-173-9	Sequence 9, Appli
36	547	39.8	223	2	US-08-487-167-9	Sequence 9, Appli
37	547	39.8	223	2	US-08-482-816-9	Sequence 9, Appli
38	547	39.8	223	2	US-08-296-149-9	Sequence 9, Appli
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40	547	39.8	223	2	US-08-615-271-9	Sequence 9, Appli
41	547	39.8	223	3	US-09-074-660-9	Sequence 9, Appli
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44	547	39.8	223	3	US-09-106-466A-9	Sequence 9, Appli
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50	545	39.7	225	4	US-09-654-600A-4	Sequence 4, Appli
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52	544.5	39.6	291	2	US-08-628-198-11	Sequence 11, Appl
53	544.5	39.6	291	3	US-09-201-038-11	Sequence 11, Appl
54	544.5	39.6	291	5	PCT-US96-07343-11	Sequence 11, Appl
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56	540	39.3	224	3	US-08-944-483-33	Sequence 33, Appl
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58	529.5	38.5	225	2	US-09-154-344-12	Sequence 12, Appl
59	524	38.1	232	2	US-08-978-404B-45	Sequence 45, Appl
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75	514	37.4	268	4	US-09-764-762-1	Sequence 1, Appli
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79	503	36.6	263	3	US-09-210-084-5	Sequence 5, Appli
80	503	36.6	263	3	US-09-478-957-5	Sequence 5, Appli
81	503	36.6	263	4	US-09-764-762-5	Sequence 5, Appli
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84	498	36.2	254	4	US-09-636-215-525	Sequence 525, App
85	498	36.2	254	4	US-09-685-166A-525	Sequence 525, App
86	498	36.2	254	4	US-09-679-426-525	Sequence 525, App
87	498	36.2	254	4	US-09-759-143-525	Sequence 525, App
88	498	36.2	254	4	US-09-651-236-525	Sequence 525, App
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93	497	36.2	258	1	US-09-102-732-3	Sequence 3, Appli
94	497	36.2	258	3	US-09-261-767-3	Sequence 3, Appli
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97	496.5	36.1	248	3	US-09-102-732-1	Sequence 1, Appli
98	496.5	36.1	248	3	US-09-261-767-1	Sequence 1, Appli
99	494	36.0	254	3	US-09-439-313-523	Sequence 523, App
100	494	36.0	254	4	US-09-636-215-523	Sequence 523, App

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102	494	36.0	254	4	US-09-679-426-523	Sequence 523, App	175	458	33.3	228	2	US-08-801-499-7	Sequence 7, Appli
103	494	36.0	254	4	US-09-759-143-523	Sequence 523, App	176	458	33.3	228	2	US-08-615-271-7	Sequence 7, Appli
104	494	36.0	254	4	US-09-651-236-523	Sequence 523, App	177	458	33.3	228	3	US-09-074-660-7	Sequence 7, Appli
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106	493	35.9	262	2	US-08-790-137-3	Sequence 3, Appli	179	458	33.3	228	3	US-09-106-468-7	Sequence 7, Appli
107	493	35.9	262	2	US-08-681-151-4	Sequence 4, Appli	180	458	33.3	228	3	US-09-106-466A-7	Sequence 7, Appli
108	493	35.9	262	2	US-08-824-874-4	Sequence 4, Appli	181	458	33.3	228	3	US-09-106-467-7	Sequence 7, Appli
109	493	35.9	262	3	US-08-807-151-4	Sequence 4, Appli	182	457.5	33.3	237	3	US-08-768-859A-1	Sequence 1, Appli
110	493	35.9	262	3	US-09-210-084-4	Sequence 4, Appli	183	457.5	33.3	237	3	US-08-767-820A-1	Sequence 1, Appli
111	493	35.9	262	3	US-09-478-957-4	Sequence 4, Appli	184	457.5	33.3	237	3	US-08-622-046B-7	Sequence 7, Appli
112	493	35.9	262	4	US-09-764-762-4	Sequence 4, Appli	185	457.5	33.3	237	3	US-08-944-483-38	Sequence 38, Appl
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114	492	35.8	225	4	US-09-644-600-5	Sequence 5, Appli	187	457.5	33.3	237	4	US-09-303-339-2	Sequence 2, Appli
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117	492	35.8	262	2	US-09-102-732-4	Sequence 4, Appli	190	455.5	33.2	237	1	US-08-096-946-11	Sequence 11, Appl
118	492	35.8	262	3	US-09-261-767-4	Sequence 4, Appli	191	455.5	33.2	237	5	PCT-US94-07329-11	Sequence 11, Appl
119	491	35.7	221	4	US-09-959-392-33	Sequence 33, Appl	192	455.5	33.2	237	5	PCT-US95-06157-1	Sequence 1, Appli
120	490	35.7	224	3	US-08-944-483-34	Sequence 34, Appl	193	455.5	33.2	261	3	US-08-768-859A-19	Sequence 19, Appl
121	487.5	35.5	449	4	US-09-636-215-617	Sequence 617, App	194	455.5	33.2	261	3	US-08-767-820A-19	Sequence 19, Appl
122	487.5	35.5	449	4	US-09-685-166A-617	Sequence 617, App	195	455.5	33.2	261	3	US-08-622-046B-3	Sequence 3, Appli
123	487.5	35.5	449	4	US-09-679-426-617	Sequence 617, App	196	454.5	33.1	232	2	US-08-897-340-31	Sequence 31, Appl
124	487.5	35.5	449	4	US-09-759-143-617	Sequence 617, App	197	454.5	33.1	232	3	US-09-252-329-31	Sequence 31, Appl
125	487.5	35.5	449	4	US-09-651-236-617	Sequence 617, App	198	454.5	33.1	244	5	PCT-US95-06157-10	Sequence 10, Appl
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127	487	35.4	224	3	US-08-944-483-36	Sequence 13, Appl	200	452.5	32.9	244	3	US-08-768-859A-10	Sequence 10, Appl
128	487	35.4	224	3	US-09-296-219-13	Sequence 36, Appl	201	452.5	32.9	244	3	US-08-767-820A-10	Sequence 10, Appl
129	478	34.8	224	3	US-08-944-483-35	Sequence 35, Appl	202	452.5	32.9	244	3	US-08-622-046B-16	Sequence 16, Appl
130	472.5	34.4	220	3	US-09-439-313-327	Sequence 327, App	203	452.5	32.9	244	3	US-09-100-264-5	Sequence 5, Appli
131	472.5	34.4	220	3	US-09-352-616A-327	Sequence 327, App	204	452.5	32.8	237	2	US-08-843-076D-5	Sequence 2, Appli
132	472.5	34.4	220	4	US-09-232-149A-327	Sequence 327, App	205	450.5	32.8	244	2	US-08-844-024-2	Sequence 2, Appli
133	472.5	34.4	220	4	US-09-636-215-327	Sequence 327, App	206	450.5	32.8	237	2	US-08-718-547-2	Sequence 2, Appli
134	472.5	34.4	220	4	US-09-685-166A-327	Sequence 327, App	207	450.5	32.8	237	3	US-08-768-859A-16	Sequence 16, Appl
135	472.5	34.4	220	4	US-09-688-489-327	Sequence 327, App	208	450.5	32.8	237	3	US-08-767-820A-16	Sequence 16, Appl
136	472.5	34.4	220	4	US-09-679-426-327	Sequence 327, App	209	450.5	32.8	237	3	US-08-622-046B-12	Sequence 12, Appl
137	472.5	34.4	220	4	US-09-759-143-327	Sequence 327, App	210	450.5	32.8	237	3	US-08-944-483-37	Sequence 37, Appl
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139	472.5	34.4	262	4	US-09-618-259-9	Sequence 9, Appli	212	450.5	32.8	237	4	US-08-843-076D-1	Sequence 1, Appli
140	470.5	34.2	261	1	US-08-744-026-5	Sequence 5, Appli	213	450.5	32.8	238	3	US-08-768-859A-8	Sequence 8, Appli
141	470.5	34.2	261	2	US-09-102-732-5	Sequence 5, Appli	214	450.5	32.8	238	3	US-08-767-820A-8	Sequence 8, Appli
142	470.5	34.2	261	3	US-09-083-521-6	Sequence 6, Appli	215	450	32.8	260	3	US-08-983-075D-9	Sequence 9, Appli
143	470.5	34.2	261	3	US-09-261-767-5	Sequence 5, Appli	216	449.5	32.7	244	3	US-08-622-046B-5	Sequence 5, Appli
144	470.5	34.2	261	4	US-09-413-049-1	Sequence 1, Appli	217	448.5	32.6	237	1	US-08-096-946-10	Sequence 10, Appl
145	470.5	34.2	261	4	US-09-907-402-1	Sequence 10, Appl	218	448.5	32.6	237	5	PCT-US94-07329-10	Sequence 10, Appl
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149	469.5	34.2	271	1	US-08-467-155A-10	Sequence 10, Appl	222	447.5	32.6	237	3	US-08-622-046B-1	Sequence 1, Appli
150	469.5	34.2	271	2	US-08-628-198-10	Sequence 10, Appl	223	447.5	32.6	237	3	US-09-100-264-12	Sequence 12, Appl
151	469.5	34.2	271	3	US-09-201-038-10	Sequence 10, Appl	224	447.5	32.6	237	4	US-08-843-076D-8	Sequence 8, Appli
152	469.5	34.2	271	5	PCT-US96-07343-10	Sequence 10, Appl	225	445	32.4	240	1	US-08-472-228A-1	Sequence 1, Appli
153	469	34.1	284	4	US-09-386-642-54	Sequence 54, Appl	226	445	32.4	240	3	US-09-146-831-1	Sequence 1, Appli
154	464.5	33.8	286	1	US-08-467-155A-9	Sequence 9, Appli	227	445	32.4	240	5	PCT-US96-09303-1	Sequence 1, Appli
155	464.5	33.8	286	2	US-08-628-198-9	Sequence 9, Appli	228	430	31.3	299	1	US-08-467-155A-8	Sequence 8, Appli
156	464.5	33.8	286	3	US-09-201-038-9	Sequence 9, Appli	229	430	31.3	299	2	US-08-628-198-8	Sequence 8, Appli
157	464.5	33.8	286	5	PCT-US96-07343-9	Sequence 9, Appli	230	430	31.3	299	3	US-09-201-038-8	Sequence 8, Appli
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168	458.5	33.4	278	4	US-09-949-016-7711	Sequence 7711, Ap	241	426.5	31.0	205	4	US-09-688-489-176	Sequence 176, App
169	458	33.3	228	1	US-08-278-091-7	Sequence 7, Appli	242	426.5	31.0	205	4	US-09-679-426-176	Sequence 176, App
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173	458	33.3	228	2	US-08-482-816-7	Sequence 7, Appli	246	417.5	30.4	233	2	US-08-738-413B-9	Sequence 9, Appli

247	406.5	29.6	231	4	US-09-402-515A-16	Sequence 16, Appl	320	354	25.8	461	6	5270178-18	Patent No. 5270178
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251	387	28.2	253	6	5223425-8	Patent No. 5223425	324	353.5	25.7	270	2	US-08-978-404B-8	Sequence 8, Appli
252	387	28.2	253	6	5223425-8	Patent No. 5223425	325	353	25.7	274	2	US-08-978-404B-5	Sequence 5, Appli
253	385.5	28.1	267	4	US-09-949-016-9575	Sequence 9575, Ap	326	353	25.7	314	3	US-09-008-271A-3	Sequence 3, Appli
254	385	28.0	232	2	US-08-738-413B-11	Sequence 11, Appl	327	353	25.7	314	4	US-09-023-942A-6	Sequence 6, Appli
255	385	28.0	250	6	5223425-4	Patent No. 5223425	328	353	25.7	314	4	US-09-907-794A-257	Sequence 257, App
256	385	28.0	250	6	5223425-4	Patent No. 5223425	329	353	25.7	314	4	US-09-905-125A-257	Sequence 257, App
257	377.5	27.5	154	3	US-09-261-416-5	Sequence 5, Appli	330	353	25.7	314	4	US-09-902-775A-257	Sequence 257, App
258	374.5	27.3	238	6	5223425-5	Patent No. 5223425	331	353	25.7	314	4	US-09-906-700-257	Sequence 257, App
259	374.5	27.3	238	6	5223425-5	Patent No. 5223425	332	353	25.7	314	4	US-09-903-603A-257	Sequence 257, App
260	374.5	27.3	259	6	5223425-2	Patent No. 5223425	333	353	25.7	314	4	US-09-904-920A-257	Sequence 257, App
261	374.5	27.3	259	6	5223425-2	Patent No. 5223425	334	353	25.7	314	4	US-09-909-064-257	Sequence 257, App
262	374	27.2	260	6	5223425-10	Patent No. 5223425	335	353	25.7	314	4	US-09-905-381A-257	Sequence 257, App
263	374	27.2	260	6	5223425-10	Patent No. 5223425	336	353	25.7	314	4	US-09-906-618-257	Sequence 257, App
264	370.5	27.0	228	3	US-08-944-483-44	Sequence 44, Appl	337	351.5	25.6	814	1	US-08-750-711-1	Sequence 1, Appli
265	370	26.9	418	4	US-09-370-838-62	Sequence 62, Appl	338	349.5	25.4	166	4	US-09-636-215-838	Sequence 838, App
266	370	26.9	418	4	US-09-854-133-62	Sequence 62, Appl	339	349.5	25.4	166	4	US-09-685-166A-838	Sequence 838, App
267	368	26.8	418	1	US-08-508-448C-25	Sequence 25, Appl	340	349.5	25.4	166	4	US-09-679-426-838	Sequence 838, App
268	368	26.8	418	4	US-09-370-838-82	Sequence 82, Appl	341	349.5	25.4	166	4	US-09-759-143-838	Sequence 838, App
269	368	26.8	418	4	US-09-370-838-83	Sequence 83, Appl	342	349.5	25.4	166	4	US-09-651-236-838	Sequence 838, App
270	368	26.8	418	4	US-09-854-133-82	Sequence 82, Appl	343	349	25.4	159	3	US-09-020-956-172	Sequence 172, App
271	368	26.8	418	4	US-09-854-133-83	Sequence 83, Appl	344	349	25.4	159	3	US-09-030-607-172	Sequence 172, App
272	366.5	26.7	149	3	US-09-518-046-20	Sequence 20, Appl	345	349	25.4	159	3	US-09-439-313-172	Sequence 172, App
273	366	26.6	232	1	US-08-508-448C-19	Sequence 19, Appl	346	349	25.4	159	3	US-09-352-616A-172	Sequence 172, App
274	366	26.6	234	2	US-08-738-413B-12	Sequence 12, Appl	347	349	25.4	159	4	US-09-232-149A-172	Sequence 172, App
275	365.5	26.6	245	3	US-08-906-769-121	Sequence 121, App	348	349	25.4	159	4	US-09-159-812-172	Sequence 172, App
276	365.5	26.6	245	3	US-08-906-616-121	Sequence 121, App	349	349	25.4	159	4	US-09-636-215-172	Sequence 172, App
277	365.5	26.6	245	3	US-08-639-075A-121	Sequence 121, App	350	349	25.4	159	4	US-09-685-166A-172	Sequence 172, App
278	365.5	26.6	245	3	US-09-012-431-121	Sequence 121, App	351	349	25.4	159	4	US-09-115-453-172	Sequence 172, App
279	365.5	26.6	245	3	US-09-012-692-121	Sequence 121, App	352	349	25.4	159	4	US-09-688-489-172	Sequence 172, App
280	365.5	26.6	245	3	US-08-906-613-121	Sequence 121, App	353	349	25.4	159	4	US-09-679-426-172	Sequence 172, App
281	364.5	26.5	400	3	US-09-004-731-30	Sequence 30, Appl	354	349	25.4	159	4	US-09-759-143-172	Sequence 172, App
282	364.5	26.5	400	3	US-09-004-731-33	Sequence 33, Appl	355	349	25.4	159	4	US-09-651-236-172	Sequence 172, App
283	364.5	26.5	400	3	US-08-749-699-30	Sequence 30, Appl	356	349	25.4	1019	1	US-08-296-014A-4	Sequence 4, Appli
284	364.5	26.5	400	3	US-08-749-699-33	Sequence 33, Appl	357	349	25.4	1019	2	US-08-596-405-4	Sequence 4, Appli
285	364.5	26.5	400	4	US-09-004-729-30	Sequence 30, Appl	358	349	25.4	1019	2	US-08-877-620-4	Sequence 4, Appli
286	364.5	26.5	400	4	US-09-004-729-33	Sequence 33, Appl	359	349	25.4	1019	4	US-09-287-368-4	Sequence 4, Appli
287	362.5	26.4	242	3	US-09-004-731-36	Sequence 36, Appl	360	349	25.4	1019	4	US-09-626-795-4	Sequence 4, Appli
288	362.5	26.4	242	3	US-08-749-699-36	Sequence 36, Appl	361	349	25.4	1083	1	US-08-296-014A-2	Sequence 2, Appli
289	362.5	26.4	242	4	US-09-004-729-36	Sequence 36, Appl	362	349	25.4	1083	2	US-08-596-405-2	Sequence 2, Appli
290	362.5	26.4	319	4	US-09-386-642-12	Sequence 12, Appl	363	349	25.4	1083	2	US-08-877-620-2	Sequence 2, Appli
291	362.5	26.4	328	4	US-09-386-642-11	Sequence 11, Appl	364	349	25.4	1083	4	US-09-287-368-2	Sequence 2, Appli
292	361.5	26.3	387	3	US-09-032-215-8	Sequence 8, Appli	365	349	25.4	1083	4	US-09-626-795-2	Sequence 2, Appli
293	361.5	26.3	387	3	US-09-032-215-13	Sequence 13, Appl	366	348	25.3	461	6	5460953-3	Patent No. 5460953
294	361	26.3	236	1	US-08-684-862-4	Sequence 4, Appli	367	348	25.3	461	6	5460953-3	Patent No. 5460953
295	360.5	26.2	299	3	US-08-944-483-66	Sequence 66, Appl	368	347	25.3	262	1	US-07-720-189-1	Sequence 1, Appli
296	358.5	26.1	232	4	US-09-959-392-31	Sequence 31, Appl	369	347	25.3	356	4	US-09-054-272-18	Sequence 18, Appl
297	358	26.1	812	4	US-08-991-761A-7	Sequence 7, Appli	370	347	25.3	356	4	US-09-065-872-2	Sequence 2, Appli
298	357.5	26.0	232	3	US-08-906-769-81	Sequence 81, Appl	371	347	25.3	409	3	US-09-667-570A-2	Sequence 2, Appli
299	357.5	26.0	232	3	US-08-906-616-81	Sequence 81, Appl	372	347	25.3	409	4	US-09-065-872-1	Sequence 1, Appli
300	357.5	26.0	232	3	US-08-817-795-81	Sequence 81, Appl	373	347	25.3	410	3	US-09-667-570A-1	Sequence 1, Appli
301	357.5	26.0	232	3	US-08-639-075A-81	Sequence 81, Appl	374	347	25.3	419	1	US-08-295-411-1	Sequence 1, Appli
302	357.5	26.0	232	3	US-09-012-431-81	Sequence 81, Appl	375	347	25.3	419	2	US-08-955-471-1	Sequence 1, Appli
303	357.5	26.0	232	3	US-09-012-692-81	Sequence 81, Appl	376	347	25.3	419	4	US-09-667-570A-3	Sequence 3, Appli
304	357.5	26.0	232	3	US-08-906-613-81	Sequence 81, Appl	377	347	25.3	419	4	US-10-182-263-1	Sequence 1, Appli
305	357.5	26.0	232	5	PCT-US95-14442A-81	Sequence 81, Appl	378	347	25.3	419	5	PCT-US92-10242-1	Sequence 1, Appli
306	357	26.0	268	4	US-09-949-016-10712	Sequence 10712, A	379	347	25.3	460	2	US-08-756-506-2	Sequence 2, Appli
307	356.5	25.9	248	3	US-08-944-483-63	Sequence 63, Appl	380	347	25.3	460	2	US-08-756-506-4	Sequence 4, Appli
308	355.5	25.9	148	4	US-09-618-259-2	Sequence 2, Appli	381	347	25.3	461	4	US-10-182-263-2	Sequence 2, Appli
309	355.5	25.9	231	2	US-09-027-337-6	Sequence 6, Appli	382	347	25.3	461	4	US-09-054-272-32	Sequence 32, Appl
310	355.5	25.9	231	4	US-09-644-600-6	Sequence 6, Appli	383	347	25.3	461	4	US-09-949-016-5921	Sequence 5921, Ap
311	355.5	25.9	231	4	US-09-654-600A-6	Sequence 6, Appli	384	347	25.3	461	6	5225537-2	Patent No. 5225537
312	355.5	25.9	276	2	US-09-016-366A-15	Sequence 15, Appl	385	347	25.3	461	6	5225537-2	Patent No. 5225537
313	355.5	25.9	276	2	US-08-978-404B-21	Sequence 21, Appl	386	347	25.3	485	4	US-09-949-016-10882	Sequence 10882, A
314	354.5	25.8	461	6	5270178-2	Patent No. 5270178	387	346.5	25.2	791	1	US-08-643-219-1	Sequence 1, Appli
315	354.5	25.8	461	6	5270178-2	Patent No. 5270178	388	346.5	25.2	791	3	US-08-851-350-1	Sequence 1, Appli
316	354	25.8	229	2	US-08-557-146-13	Sequence 13, Appl	389	346	25.2	234	3	US-08-944-483-46	Sequence 46, Appl
317	354	25.8	229	2	US-09-154-344-13	Sequence 13, Appl	390	346	25.2	241	3	US-08-944-483-59	Sequence 59, Appl
318	354	25.8	312	4	US-09-023-942A-4	Sequence 4, Appli	391	346	25.2	419	4	US-10-182-263-5	Sequence 5, Appli
319	354	25.8	461	6	5270178-17	Patent No. 5270178	392	346	25.2	419	4	US-10-182-263-6	Sequence 6, Appli



393	345.5	25.1	248	3	US-08-906-769-111	Sequence 111, App	466	339.5	24.7	253	3	US-09-578-303-4	Sequence 4, Appli
394	345.5	25.1	248	3	US-08-906-616-111	Sequence 111, App	467	339.5	24.7	258	1	US-07-990-301A-2	Sequence 2, Appli
395	345.5	25.1	248	3	US-08-817-795-111	Sequence 111, App	468	339.5	24.7	333	4	US-08-991-761A-8	Sequence 8, Appli
396	345.5	25.1	248	3	US-08-639-075A-111	Sequence 111, App	469	339	24.7	419	4	US-10-182-263-4	Sequence 4, Appli
397	345.5	25.1	248	3	US-09-012-431-111	Sequence 111, App	470	339	24.7	461	3	US-08-742-877-2	Sequence 2, Appli
398	345.5	25.1	248	3	US-09-012-692-111	Sequence 111, App	471	339	24.7	461	3	US-09-053-871A-21	Sequence 21, Appl
399	345.5	25.1	248	3	US-08-906-613-111	Sequence 111, App	472	339	24.7	461	4	US-10-133-907-5	Sequence 5, Appli
400	345.5	25.1	248	5	PCT-US95-14442A-111	Sequence 111, App	473	339	24.7	461	6	5521070-2	Patent No. 5521070
401	344	25.0	274	2	US-09-016-366A-21	Sequence 21, Appl	474	339	24.7	461	6	5521070-2	Patent No. 5521070
402	344	25.0	274	2	US-08-978-404B-16	Sequence 16, Appl	475	339	24.7	480	4	US-09-949-016-11123	Sequence 11123, A
403	343.5	25.0	273	2	US-08-978-404B-3	Sequence 3, Appli	476	339	24.7	481	4	US-09-949-016-9238	Sequence 9238, Ap
404	343.5	25.0	460	6	5270178-13	Patent No. 5270178	477	339	24.7	637	4	US-09-949-016-9239	Sequence 9239, Ap
405	343.5	25.0	460	6	5270178-14	Patent No. 5270178	478	339	24.7	637	4	US-09-949-016-11538	Sequence 11538, A
406	343.5	25.0	460	6	5270178-15	Patent No. 5270178	479	339	24.7	637	4	US-09-949-016-11539	Sequence 11539, A
407	343.5	25.0	460	6	5270178-16	Patent No. 5270178	480	338.5	24.6	230	1	US-08-379-621-2	Sequence 2, Appli
408	343.5	25.0	460	6	5270178-13	Patent No. 5270178	481	338.5	24.6	230	1	US-08-147-000B-2	Sequence 2, Appli
409	343.5	25.0	460	6	5270178-14	Patent No. 5270178	482	338.5	24.6	230	2	US-08-889-078-2	Sequence 2, Appli
410	343.5	25.0	460	6	5270178-15	Patent No. 5270178	483	338.5	24.6	261	6	5270178-5	Patent No. 5270178
411	343.5	25.0	460	6	5270178-16	Patent No. 5270178	484	338.5	24.6	261	6	5270178-5	Patent No. 5270178
412	343	25.0	284	4	US-09-387-375-7	Sequence 7, Appli	485	338.5	24.6	308	3	US-08-705-875A-10	Sequence 10, Appl
413	343	25.0	284	4	US-10-041-400A-7	Sequence 7, Appli	486	338.5	24.6	308	4	US-09-242-999-10	Sequence 10, Appl
414	343	25.0	284	4	US-10-042-091A-7	Sequence 7, Appli	487	338	24.6	250	3	US-08-944-483-51	Sequence 51, Appl
415	342.5	24.9	248	3	US-09-032-215-37	Sequence 37, Appl	488	337.5	24.6	267	4	US-09-949-016-10711	Sequence 10711, A
416	342.5	24.9	249	3	US-09-042-215-37	Sequence 5, Appli	489	337	24.5	235	3	US-08-944-483-48	Sequence 48, Appl
417	342.5	24.9	273	2	US-09-079-970A-5	Sequence 6, Appli	490	337	24.5	406	4	US-09-851-588-6	Sequence 6, Appli
418	342.5	24.9	546	6	5200340-6	Patent No. 5200340	491	337	24.5	423	4	US-09-656-002-2	Sequence 2, Appli
419	342.5	24.9	546	6	5200340-6	Patent No. 5200340	492	337	24.5	435	4	US-09-607-745-2	Sequence 2, Appli
420	342.5	24.9	713	4	US-09-949-016-9983	Sequence 9983, Ap	493	337	24.5	437	4	US-09-851-588-8	Sequence 8, Appli
421	342.5	24.9	790	1	US-08-469-486-54	Sequence 54, Appl	494	337	24.5	812	1	US-08-248-629A-1	Sequence 1, Appli
422	342.5	24.9	790	2	US-08-469-658-54	Sequence 54, Appl	495	337	24.5	812	1	US-08-451-932-1	Sequence 1, Appli
423	342.5	24.9	791	2	US-09-131-995-1	Sequence 1, Appli	496	337	24.5	812	1	US-08-452-260-1	Sequence 1, Appli
424	342.5	24.9	791	2	US-08-832-087B-1	Sequence 1, Appli	497	337	24.5	812	1	US-08-326-785-1	Sequence 1, Appli
425	342.5	24.9	791	3	US-09-132-154-1	Sequence 1, Appli	498	337	24.5	812	2	US-08-612-788-1	Sequence 1, Appli
426	342.5	24.9	791	4	US-08-991-761A-6	Sequence 6, Appli	499	337	24.5	812	2	US-08-605-598B-1	Sequence 1, Appli
427	342.5	24.9	791	4	US-08-924-287A-1	Sequence 1, Appli	500	337	24.5	812	2	US-08-429-743-1	Sequence 1, Appli
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429	342.5	24.9	810	1	US-08-147-000B-29	Sequence 29, Appl	502	337	24.5	812	3	US-09-066-028-1	Sequence 1, Appli
430	342.5	24.9	810	3	US-09-086-514-1	Sequence 1, Appli	503	337	24.5	812	4	US-09-335-325-1	Sequence 3, Appli
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432	342.5	24.9	810	4	US-09-403-736-1	Sequence 1, Appli	505	337	24.5	812	4	US-08-991-761A-12	Sequence 12, Appl
433	342.5	24.9	810	4	US-09-701-265-1	Sequence 1, Appli	506	337	24.5	812	5	PCT-US95-05107-1	Sequence 1, Appli
434	342.5	24.9	810	6	5200340-8	Patent No. 5200340	507	336.5	24.5	435	3	US-09-008-271A-6	Sequence 6, Appli
435	342.5	24.9	810	6	5200340-8	Patent No. 5200340	508	336	24.5	415	1	US-08-073-531B-1	Sequence 1, Appli
436	342	24.9	234	1	US-08-684-862-3	Sequence 3, Appli	509	336	24.5	415	2	US-08-766-288-1	Sequence 1, Appli
437	342	24.9	273	2	US-09-016-366A-19	Sequence 19, Appl	510	336	24.5	790	4	US-08-991-761A-13	Sequence 13, Appl
438	342	24.9	273	2	US-08-978-404B-14	Sequence 14, Appl	511	334.5	24.3	446	4	US-10-177-661-4	Sequence 4, Appli
439	341.5	24.9	156	3	US-09-261-416-6	Sequence 6, Appli	512	334.5	24.3	477	4	US-10-177-661-2	Sequence 2, Appli
440	341.5	24.9	261	6	5270178-19	Patent No. 5270178	513	334.5	24.3	562	4	US-09-879-792-12	Sequence 12, Appl
441	341.5	24.9	261	6	5270178-20	Patent No. 5270178	514	334	24.3	316	4	US-09-387-375-9	Sequence 9, Appli
442	341.5	24.9	261	6	5270178-19	Patent No. 5270178	515	334	24.3	316	4	US-10-041-400A-9	Sequence 9, Appli
443	341.5	24.9	261	6	5270178-20	Patent No. 5270178	516	334	24.3	316	4	US-10-042-091A-9	Sequence 9, Appli
444	341	24.8	261	6	5270178-21	Patent No. 5270178	517	333.5	24.3	290	4	US-09-386-653A-7	Sequence 7, Appli
445	341	24.8	261	6	5270178-21	Patent No. 5270178	518	333.5	24.3	302	3	US-09-220-731-26	Sequence 26, Appl
446	341	24.8	306	4	US-09-386-642-53	Sequence 53, Appl	519	333.5	24.3	302	4	US-09-242-999-22	Sequence 22, Appl
447	341	24.8	415	4	US-09-118-748-2	Sequence 2, Appli	520	333	24.2	415	1	US-08-295-411-2	Sequence 2, Appli
448	340.5	24.8	230	1	US-08-456-840-47	Sequence 47, Appl	521	333	24.2	415	2	US-08-955-471-2	Sequence 2, Appli
449	340.5	24.8	230	1	US-08-266-407A-47	Sequence 47, Appl	522	333	24.2	415	5	PCT-US92-10242-2	Sequence 2, Appli
450	340.5	24.8	230	2	US-08-892-544-47	Sequence 47, Appl	523	332.5	24.2	638	2	US-08-681-151-3	Sequence 3, Appli
451	340.5	24.8	230	2	US-08-766-982-12	Sequence 12, Appl	524	332.5	24.2	810	4	US-08-991-761A-11	Sequence 11, Appl
452	340.5	24.8	230	3	US-08-944-483-53	Sequence 53, Appl	525	331	24.1	295	3	US-08-338-368-2	Sequence 2, Appli
453	340.5	24.8	230	3	US-09-296-219-12	Sequence 12, Appl	526	331	24.1	579	1	US-08-295-411-4	Sequence 4, Appli
454	340.5	24.8	244	4	US-09-601-318-4	Sequence 4, Appli	527	331	24.1	579	2	US-08-955-471-4	Sequence 4, Appli
455	340.5	24.8	244	4	US-09-601-318-5	Sequence 5, Appli	528	331	24.1	579	3	US-09-117-708-14	Sequence 14, Appl
456	340.5	24.8	244	4	US-09-601-318-6	Sequence 6, Appli	529	331	24.1	579	5	PCT-US92-10242-4	Sequence 4, Appli
457	340.5	24.8	244	4	US-09-601-318-7	Sequence 7, Appli	530	331	24.1	615	1	US-07-998-972A-3	Sequence 3, Appli
458	340.5	24.8	245	3	US-09-079-970A-6	Sequence 6, Appli	531	331	24.1	615	1	US-08-463-953-3	Sequence 3, Appli
459	340.5	24.8	245	4	US-09-601-318-1	Sequence 1, Appli	532	331	24.1	615	1	US-08-462-261-3	Sequence 3, Appli
460	340.5	24.8	267	2	US-09-016-366A-23	Sequence 23, Appl	533	331	24.1	615	5	PCT-US92-11357-3	Sequence 3, Appli
461	340.5	24.8	267	2	US-08-978-404B-18	Sequence 18, Appl	534	331	24.1	622	3	US-08-952-967-8	Sequence 8, Appli
462	340.5	24.8	267	4	US-09-917-254-101	Sequence 101, App	535	331	24.1	560	4	US-09-054-272-42	Sequence 42, Appl
463	340.5	24.8	300	3	US-08-705-875A-6	Sequence 6, Appli	536	330.5	24.1	560	4	US-09-949-016-6458	Sequence 6458, Ap
464	340.5	24.8	300	4	US-08-242-999-6	Sequence 6, Appli	537	330.5	24.1	560	4	US-09-912-559-3	Sequence 3, Appli
465	340	24.7	419	4	US-10-182-263-3	Sequence 3, Appli	538	330	24.0	221	3	US-08-944-483-54	Sequence 54, Appl



539	330	24.0	222	1	US-08-456-840-46	Sequence 46, Appl	612	321	23.4	300	1	US-08-448-937A-1	Sequence 1, Appli
540	330	24.0	222	1	US-08-266-407A-46	Sequence 46, Appl	613	321	23.4	315	4	US-09-386-653A-9	Sequence 9, Appli
541	330	24.0	222	2	US-08-892-544-46	Sequence 46, Appl	614	321	23.4	655	1	US-08-148-910-12	Sequence 12, Appl
542	330	24.0	222	6	5223425-6	Patent No. 5223425	615	321	23.4	655	1	US-08-448-937A-12	Sequence 12, Appl
543	330	24.0	222	6	5223425-6	Patent No. 5223425	616	321	23.4	809	4	US-08-991-761A-9	Sequence 9, Appli
544	329.5	24.0	230	4	US-09-601-318-3	Sequence 3, Appli	617	319.5	23.3	240	1	US-08-278-091-11	Sequence 11, Appl
545	329.5	24.0	376	2	US-08-558-269-10	Sequence 10, Appl	618	319.5	23.3	240	1	US-08-483-859-11	Sequence 11, Appl
546	329.5	24.0	376	3	US-09-410-882-10	Sequence 10, Appl	619	319.5	23.3	240	1	US-08-472-173-11	Sequence 11, Appl
547	329	23.9	259	3	US-08-944-483-52	Sequence 52, Appl	620	319.5	23.3	240	2	US-08-487-167-11	Sequence 11, Appl
548	328.5	23.9	238	3	US-08-944-483-64	Sequence 64, Appl	621	319.5	23.3	240	2	US-08-482-816-11	Sequence 11, Appl
549	328.5	23.9	338	4	US-08-991-761A-10	Sequence 10, Appl	622	319.5	23.3	240	2	US-08-296-149-11	Sequence 11, Appl
550	327.5	23.8	151	3	US-09-518-046-21	Sequence 21, Appl	623	319.5	23.3	240	2	US-08-801-499-11	Sequence 11, Appl
551	327.5	23.8	154	3	US-09-261-416-7	Sequence 7, Appli	624	319.5	23.3	240	2	US-08-615-271-11	Sequence 11, Appl
552	327	23.8	241	3	US-08-944-483-60	Sequence 60, Appl	625	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
553	327	23.8	255	1	US-08-650-129-5	Sequence 5, Appli	626	319.5	23.3	240	3	US-09-074-659-11	Sequence 11, Appl
554	327	23.8	255	3	US-08-984-417-5	Sequence 5, Appli	627	319.5	23.3	240	3	US-09-106-468-11	Sequence 11, Appl
555	326.5	23.8	144	4	US-09-618-259-1	Sequence 1, Appli	628	319.5	23.3	240	3	US-09-106-466A-11	Sequence 11, Appl
556	325.5	23.7	261	3	US-08-163-919A-2	Sequence 2, Appli	629	319.5	23.3	240	3	US-09-106-467-11	Sequence 11, Appl
557	325.5	23.7	261	4	US-08-462-515-2	Sequence 2, Appli	630	319.5	23.3	254	3	US-08-944-483-50	Sequence 50, Appl
558	325.5	23.7	261	5	PCT-US94-14073-2	Sequence 2, Appli	631	318	23.1	295	4	US-10-165-442-3	Sequence 3, Appli
559	325	23.7	226	1	US-08-650-129-4	Sequence 4, Appli	632	317.5	23.1	245	3	US-08-944-483-69	Sequence 69, Appl
560	325	23.7	226	3	US-08-984-417-4	Sequence 4, Appli	633	317	23.1	232	3	US-08-944-483-45	Sequence 45, Appl
561	324.5	23.6	228	1	US-08-278-091-10	Sequence 10, Appl	634	317	23.1	295	4	US-10-165-442-1	Sequence 1, Appli
562	324.5	23.6	228	1	US-08-483-859-10	Sequence 10, Appl	635	316.5	23.0	226	1	US-07-929-198-2	Sequence 2, Appli
563	324.5	23.6	228	1	US-08-472-173-10	Sequence 10, Appl	636	316.5	23.0	226	1	US-07-929-198-6	Sequence 6, Appli
564	324.5	23.6	228	2	US-08-487-167-10	Sequence 10, Appl	637	316.5	23.0	226	2	US-08-557-146-15	Sequence 15, Appl
565	324.5	23.6	228	2	US-08-482-816-10	Sequence 10, Appl	638	316.5	23.0	226	2	US-09-154-344-15	Sequence 15, Appl
566	324.5	23.6	228	2	US-08-296-149-10	Sequence 10, Appl	639	316.5	23.0	226	3	US-08-944-483-43	Sequence 43, Appl
567	324.5	23.6	228	2	US-08-801-499-10	Sequence 10, Appl	640	316	23.0	246	3	US-08-906-769-127	Sequence 127, App
568	324.5	23.6	228	2	US-08-615-271-10	Sequence 10, Appl	641	316	23.0	246	3	US-08-906-616-127	Sequence 127, App
569	324.5	23.6	228	3	US-09-074-659-10	Sequence 10, Appl	642	316	23.0	246	3	US-08-639-075A-127	Sequence 127, App
570	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	643	316	23.0	246	3	US-09-012-431-127	Sequence 127, App
571	324.5	23.6	228	3	US-09-106-468-10	Sequence 10, Appl	644	316	23.0	246	3	US-09-012-692-127	Sequence 127, App
572	324.5	23.6	228	3	US-09-106-466A-10	Sequence 10, Appl	645	316	23.0	246	3	US-08-906-613-127	Sequence 127, App
573	324.5	23.6	228	3	US-09-106-467-10	Sequence 10, Appl	646	316	23.0	259	4	US-10-165-442-4	Sequence 4, Appli
574	323.5	23.5	275	2	US-09-016-366A-17	Sequence 17, Appl	647	315.5	23.0	254	3	US-09-578-303-5	Sequence 5, Appli
575	323.5	23.5	275	2	US-08-978-404B-12	Sequence 12, Appl	648	315.5	23.0	292	4	US-09-607-745-9	Sequence 9, Appli
576	323.5	23.5	406	1	US-08-293-778-24	Sequence 24, Appl	649	315.5	23.0	300	3	US-08-705-875A-4	Sequence 4, Appli
577	323.5	23.5	406	1	US-08-295-411-5	Sequence 5, Appli	650	315.5	23.0	300	3	US-09-220-731-21	Sequence 21, Appl
578	323.5	23.5	406	2	US-08-955-471-5	Sequence 5, Appli	651	315.5	23.0	300	4	US-09-242-999-4	Sequence 4, Appli
579	323.5	23.5	406	4	US-09-782-587B-1	Sequence 1, Appli	652	315.5	23.0	487	1	US-08-469-486-53	Sequence 53, Appl
580	323.5	23.5	406	4	US-09-782-587B-3	Sequence 3, Appli	653	315.5	23.0	487	2	US-08-469-658-53	Sequence 53, Appl
581	323.5	23.5	406	5	PCT-US92-10242-5	Sequence 5, Appli	654	315.5	23.0	492	1	US-08-469-486-2	Sequence 2, Appli
582	323.5	23.5	444	1	US-08-475-845-2	Sequence 2, Appli	655	315.5	23.0	492	2	US-08-469-658-2	Sequence 2, Appli
583	323.5	23.5	444	2	US-08-327-690-2	Sequence 2, Appli	656	315	22.9	259	4	US-10-165-442-2	Sequence 2, Appli
584	323.5	23.5	444	2	US-08-660-289-2	Sequence 2, Appli	657	315	22.9	691	4	US-09-949-016-7775	Sequence 7775, Ap
585	323.5	23.5	444	2	US-08-537-807-2	Sequence 2, Appli	658	314.5	22.9	283	4	US-09-244-111-2	Sequence 2, Appli
586	323.5	23.5	444	2	US-08-871-003-2	Sequence 2, Appli	659	314	22.9	855	2	US-09-027-337-2	Sequence 2, Appli
587	323.5	23.5	444	3	US-08-464-233-2	Sequence 2, Appli	660	314	22.9	855	4	US-09-644-600-2	Sequence 2, Appli
588	323.5	23.5	444	3	US-09-189-607-2	Sequence 2, Appli	661	314	22.9	855	4	US-09-654-600A-2	Sequence 2, Appli
589	323.5	23.5	444	3	US-09-378-907-2	Sequence 2, Appli	662	313.5	22.8	226	1	US-07-929-198-4	Sequence 4, Appli
590	323.5	23.5	444	5	PCT-US94-05779-2	Sequence 2, Appli	663	312.5	22.7	242	4	US-09-959-392-34	Sequence 34, Appl
591	323.5	23.5	461	4	US-09-949-016-8839	Sequence 8839, Ap	664	312	22.7	248	3	US-08-944-483-71	Sequence 71, Appl
592	323.5	23.5	466	1	US-07-882-202A-4	Sequence 4, Appli	665	311.5	22.7	251	3	US-08-944-483-47	Sequence 47, Appl
593	323.5	23.5	466	1	US-08-021-615A-4	Sequence 4, Appli	666	311	22.6	383	2	US-08-558-269-6	Sequence 6, Appli
594	323.5	23.5	466	1	US-08-321-777-4	Sequence 4, Appli	667	311	22.6	383	3	US-09-410-882-6	Sequence 6, Appli
595	323.5	23.5	466	3	US-09-009-656-14	Sequence 14, Appl	668	311	22.6	798	4	US-08-200-900A-2	Sequence 2, Appli
596	323.5	23.5	466	3	PCT-US93-04493-4	Sequence 4, Appli	669	311	22.6	798	5	PCT-US94-00616-2	Sequence 2, Appli
597	323.5	23.5	483	4	US-09-949-016-9523	Sequence 9523, Ap	670	311	22.6	798	5	US-09-192-012-9	Sequence 9, Appli
598	323.5	23.5	285	4	US-09-023-942A-26	Sequence 26, Appl	671	311	22.6	812	4	US-09-959-392-2	Sequence 2, Appli
599	322.5	23.5	560	4	US-09-912-559-4	Sequence 4, Appli	672	311	22.6	1042	4	US-09-959-392-2	Sequence 2, Appli
600	322.5	23.5	560	4	US-10-000-489-54	Sequence 54, Appl	673	310.5	22.6	247	2	US-08-978-404B-47	Sequence 47, Appl
601	322	23.4	699	4	US-09-949-016-6138	Sequence 6138, Ap	674	309.5	22.5	241	4	US-09-657-986B-2	Sequence 2, Appli
602	322	23.4	717	4	US-09-949-016-11182	Sequence 11182, A	675	309.5	22.5	492	4	US-09-685-166A-895	Sequence 895, App
603	322	23.4	255	2	US-09-027-337-7	Sequence 7, Appli	676	309.5	22.5	492	4	US-09-879-792-14	Sequence 14, Appl
604	321.5	23.4	255	4	US-09-644-600-7	Sequence 7, Appli	677	309.5	22.5	492	4	US-09-679-426-895	Sequence 895, App
605	321.5	23.4	255	4	US-09-654-600A-7	Sequence 7, Appli	678	309.5	22.5	492	4	US-09-759-143-895	Sequence 895, App
606	321.5	23.4	418	4	US-10-177-661-6	Sequence 6, Appli	679	308.5	22.5	243	3	US-08-944-483-70	Sequence 70, Appl
607	321.5	23.4	248	2	US-08-851-974-3	Sequence 3, Appli	680	308.5	22.5	319	4	US-09-270-767-42672	Sequence 42672, A
608	321	23.4	248	2	US-09-213-390-3	Sequence 3, Appli	681	308	22.4	232	4	US-09-959-392-32	Sequence 32, Appl
609	321	23.4	269	2	US-08-978-404B-10	Sequence 10, Appl	682	308	22.4	317	4	US-09-386-629-7	Sequence 7, Appli
610	321	23.4	300	1	US-08-148-910-1	Sequence 1, Appli	683	308	22.4	317	4	US-09-907-794A-263	Sequence 263, App
611	321	23.4	308	4			684	308	22.4	317	4	US-09-905-125A-263	Sequence 263, App

685	308	22.4	317	4	US-09-902-775A-263	Sequence 263, App	758	304	22.1	562	6	5185259-3	Patent No. 5185259
686	308	22.4	317	4	US-09-906-700-263	Sequence 263, App	759	304	22.1	562	6	5200340-2	Patent No. 5200340
687	308	22.4	317	4	US-09-903-603A-263	Sequence 263, App	760	304	22.1	562	6	5244676-5	Patent No. 5244676
688	308	22.4	317	4	US-09-904-920A-263	Sequence 263, App	761	304	22.1	562	6	5344773-2	Patent No. 5344773
689	308	22.4	317	4	US-09-909-064-263	Sequence 263, App	762	304	22.1	562	6	5185259-3	Patent No. 5185259
690	308	22.4	317	4	US-09-905-381A-263	Sequence 263, App	763	304	22.1	562	6	5200340-2	Patent No. 5200340
691	308	22.4	317	4	US-09-906-618-263	Sequence 263, App	764	304	22.1	562	6	5244676-5	Patent No. 5244676
692	308	22.4	356	2	US-08-681-151-1	Sequence 1, Appli	765	304	22.1	562	6	5344773-2	Patent No. 5344773
693	307.5	22.4	376	4	US-09-820-002-2	Sequence 2, Appli	766	304	22.1	587	4	US-09-949-016-11501	Sequence 11501, A
694	307	22.3	268	1	US-08-568-031-2	Sequence 2, Appli	767	303.5	22.1	234	4	US-09-513-999C-7815	Sequence 7815, Ap
695	307	22.3	268	2	US-08-966-319-2	Sequence 2, Appli	768	303.5	22.1	278	1	US-08-392-828C-4	Sequence 4, Appli
696	307	22.3	268	3	US-09-153-304-2	Sequence 2, Appli	769	303.5	22.1	278	3	US-09-330-945-4	Sequence 4, Appli
697	307	22.3	355	2	US-08-811-949-47	Sequence 47, Appl	770	303	22.1	258	4	US-09-949-016-10661	Sequence 10661, A
698	307	22.3	355	2	US-08-811-949-59	Sequence 59, Appl	771	303	22.1	355	2	US-08-811-949-53	Sequence 53, Appl
699	307	22.3	417	4	US-09-820-002-4	Sequence 4, Appli	772	303	22.1	389	2	US-08-811-949-67	Sequence 67, Appl
700	307	22.3	437	2	US-08-811-949-51	Sequence 51, Appl	773	303	22.1	437	2	US-08-811-949-55	Sequence 55, Appl
701	307	22.3	452	4	US-09-949-016-7182	Sequence 7182, Ap	774	303	22.1	527	4	US-09-600-985-1	Sequence 1, Appli
702	307	22.3	527	2	US-08-811-949-39	Sequence 39, Appl	775	302.5	22.0	1113	4	US-09-959-392-4	Sequence 4, Appli
703	306	22.3	256	2	US-09-027-337-3	Sequence 3, Appli	776	302	22.0	389	2	US-08-811-949-65	Sequence 65, Appl
704	306	22.3	256	4	US-09-644-600-3	Sequence 3, Appli	777	302	22.0	477	2	US-08-560-098A-51	Sequence 51, Appl
705	306	22.3	256	4	US-09-654-600A-3	Sequence 3, Appli	778	302	22.0	527	4	US-09-600-985-2	Sequence 2, Appli
706	306	22.3	437	2	US-08-811-949-57	Sequence 57, Appl	779	302	22.0	527	4	US-09-600-985-3	Sequence 3, Appli
707	305.5	22.2	146	4	US-09-618-259-3	Sequence 3, Appli	780	301.5	21.9	226	3	US-08-944-483-41	Sequence 41, Appl
708	305	22.2	247	2	US-08-851-974-1	Sequence 1, Appli	781	301	21.9	255	1	US-08-208-007A-14	Sequence 14, Appl
709	305	22.2	247	2	US-08-851-974-4	Sequence 4, Appli	782	301	21.9	255	3	US-08-915-095A-14	Sequence 14, Appl
710	305	22.2	247	2	US-09-213-390-1	Sequence 1, Appli	783	301	21.9	255	3	US-08-798-096-14	Sequence 14, Appl
711	305	22.2	247	2	US-09-213-390-4	Sequence 4, Appli	784	301	21.9	255	4	US-08-798-095A-14	Sequence 14, Appl
712	305	22.2	247	4	US-09-949-016-6457	Sequence 6457, Ap	785	301	21.9	255	4	US-09-953-956-14	Sequence 14, Appl
713	305	22.2	437	2	US-08-811-949-49	Sequence 49, Appl	786	301	21.9	255	4	US-08-553-125A-14	Sequence 14, Appl
714	304.5	22.2	258	3	US-09-004-731-16	Sequence 16, Appl	787	301	21.9	255	4	US-10-114-464-14	Sequence 14, Appl
715	304.5	22.2	258	3	US-09-004-731-19	Sequence 19, Appl	788	301	21.9	257	4	US-09-949-016-10662	Sequence 10662, A
716	304.5	22.2	258	3	US-08-749-699-16	Sequence 16, Appl	789	301	21.9	527	6	5520913-1	Patent No. 5520913
717	304.5	22.2	258	3	US-08-749-699-19	Sequence 19, Appl	790	301	21.9	527	6	5520913-1	Patent No. 5520913
718	304.5	22.2	258	4	US-09-004-729-16	Sequence 16, Appl	791	300	21.8	233	4	US-09-636-382A-24	Sequence 24, Appl
719	304.5	22.2	258	4	US-09-004-729-19	Sequence 19, Appl	792	298	21.7	347	2	US-08-811-949-1	Sequence 1, Appli
720	304.5	22.2	314	4	US-09-636-382A-2	Sequence 2, Appli	793	297	21.6	237	3	US-08-163-919A-3	Sequence 3, Appli
721	304.5	22.2	384	3	US-09-032-215-22	Sequence 22, Appl	794	297	21.6	237	4	US-08-462-515-3	Sequence 3, Appli
722	304.5	22.2	393	4	US-09-759-143-934	Sequence 934, App	795	297	21.6	237	5	PCT-US94-14073-3	Sequence 3, Appli
723	304.5	22.2	492	3	US-09-342-749-2	Sequence 2, Appli	796	297	21.6	252	3	US-08-944-483-72	Sequence 72, Appl
724	304.5	22.2	492	4	US-09-691-840-2	Sequence 2, Appli	797	297	21.6	253	2	US-09-027-337-8	Sequence 8, Appli
725	304.5	22.2	492	4	US-09-759-143-932	Sequence 932, App	798	297	21.6	253	4	US-09-644-600-8	Sequence 8, Appli
726	304.5	22.2	510	4	US-09-949-016-11074	Sequence 11074, A	799	297	21.6	253	4	US-09-654-600A-8	Sequence 8, Appli
727	304	22.1	232	1	US-07-990-301A-4	Sequence 4, Appli	800	297	21.6	256	3	US-09-032-215-27	Sequence 27, Appl
728	304	22.1	235	3	US-08-944-483-65	Sequence 65, Appl	801	297	21.6	323	4	US-09-880-503-7	Sequence 7, Appli
729	304	22.1	255	3	US-08-944-483-67	Sequence 67, Appl	802	297	21.6	323	4	US-08-811-949-61	Sequence 61, Appl
730	304	22.1	268	4	US-09-613-822B-2	Sequence 2, Appli	803	297	21.6	411	3	US-09-181-816-1	Sequence 1, Appli
731	304	22.1	327	4	US-09-386-629-8	Sequence 8, Appli	804	297	21.6	521	4	US-09-949-016-11081	Sequence 11081, A
732	304	22.1	355	1	US-08-137-116-1	Sequence 1, Appli	805	297	21.6	521	4	US-09-949-016-11082	Sequence 11082, A
733	304	22.1	355	1	US-08-217-618-1	Sequence 1, Appli	806	297	21.6	521	4	US-09-949-016-11083	Sequence 11083, A
734	304	22.1	355	1	US-08-427-640-2	Sequence 2, Appli	807	296.5	21.6	224	1	US-08-278-091-12	Sequence 12, Appl
735	304	22.1	355	1	US-08-427-640-6	Sequence 6, Appli	808	296.5	21.6	224	1	US-08-483-859-12	Sequence 12, Appl
736	304	22.1	355	1	US-08-217-617A-1	Sequence 1, Appli	809	296.5	21.6	224	1	US-08-472-173-12	Sequence 12, Appl
737	304	22.1	355	1	US-08-217-616-1	Sequence 1, Appli	810	296.5	21.6	224	2	US-08-487-167-12	Sequence 12, Appl
738	304	22.1	355	2	US-08-811-949-45	Sequence 45, Appl	811	296.5	21.6	224	2	US-08-482-816-12	Sequence 12, Appl
739	304	22.1	355	3	US-08-794-528-1	Sequence 1, Appli	812	296.5	21.6	224	2	US-08-296-149-12	Sequence 12, Appl
740	304	22.1	355	6	5223256-1	Patent No. 5223256	813	296.5	21.6	224	2	US-08-801-499-12	Sequence 12, Appl
741	304	22.1	355	6	5223256-1	Patent No. 5223256	814	296.5	21.6	224	2	US-08-615-271-12	Sequence 12, Appl
742	304	22.1	356	1	US-08-427-640-4	Sequence 4, Appli	815	296.5	21.6	224	3	US-09-074-660-12	Sequence 12, Appl
743	304	22.1	356	1	US-08-427-640-8	Sequence 8, Appli	816	296.5	21.6	224	3	US-09-074-659-12	Sequence 12, Appl
744	304	22.1	378	3	US-09-553-498-10	Sequence 10, Appl	817	296.5	21.6	224	3	US-09-106-468-12	Sequence 12, Appl
745	304	22.1	378	4	US-09-618-869-10	Sequence 10, Appl	818	296.5	21.6	224	3	US-09-106-466A-12	Sequence 12, Appl
746	304	22.1	433	4	US-09-949-016-8220	Sequence 8220, Ap	819	296.5	21.6	224	3	US-09-106-467-12	Sequence 12, Appl
747	304	22.1	472	2	US-08-811-949-63	Sequence 63, Appl	820	296.5	21.6	246	4	US-09-205-258-1149	Sequence 1149, Ap
748	304	22.1	527	1	US-07-609-510B-16	Sequence 16, Appl	821	296.5	21.6	254	2	US-08-560-098A-49	Sequence 49, Appl
749	304	22.1	527	4	US-09-612-314A-51	Sequence 51, Appl	822	296.5	21.6	276	4	US-09-880-503-5	Sequence 5, Appli
750	304	22.1	527	5	PCT-US91-01025A-2	Sequence 2, Appli	823	296.5	21.6	306	2	US-08-560-098A-45	Sequence 45, Appl
751	304	22.1	527	6	5185259-8	Patent No. 5185259	824	296.5	21.6	331	2	US-08-560-098A-46	Sequence 46, Appl
752	304	22.1	527	6	5185259-8	Patent No. 5185259	825	296.5	21.6	365	1	US-08-093-741-83	Sequence 83, Appl
753	304	22.1	562	2	US-08-811-949-43	Sequence 43, Appl	826	296.5	21.6	365	1	US-08-720-012-83	Sequence 83, Appl
754	304	22.1	562	2	US-08-560-098A-50	Sequence 50, Appl	827	296.5	21.6	393	2	US-08-560-098A-44	Sequence 44, Appl
755	304	22.1	562	2	US-08-883-795A-38	Sequence 38, Appl	828	296.5	21.6	393	3	US-08-967-024C-24	Sequence 24, Appl
756	304	22.1	562	4	US-09-703-695A-4	Sequence 4, Appli	829	296.5	21.6	393	3	US-08-967-024C-25	Sequence 25, Appl
757	304	22.1	562	4	US-10-443-701-4	Sequence 4, Appli	830	296.5	21.6	403	4	US-09-880-503-6	Sequence 6, Appli

831	296.5	21.6	411	1	US-08-087-163-1	Sequence 1, Appli	904	282	20.5	244	3	US-08-944-483-74	Sequence 74, Appl
832	296.5	21.6	411	1	US-08-286-748B-18	Sequence 18, Appl	905	279	20.3	902	4	US-09-644-600-10	Sequence 10, Appl
833	296.5	21.6	411	1	US-08-153-799-18	Sequence 18, Appl	906	279	20.3	902	4	US-09-654-600A-10	Sequence 10, Appl
834	296.5	21.6	411	2	US-08-560-098A-48	Sequence 48, Appl	907	277.5	20.2	242	3	US-08-944-483-58	Sequence 58, Appl
835	296.5	21.6	411	4	US-09-880-503-3	Sequence 3, Appli	908	277	20.2	488	4	US-09-367-777-44	Sequence 44, Appl
836	296.5	21.6	430	6	5219569-2	Patent No. 5219569	909	277	20.2	488	4	US-09-367-791A-27	Sequence 27, Appl
837	296.5	21.6	430	6	5219569-2	Patent No. 5219569	910	276	20.1	306	1	US-08-330-978-1	Sequence 1, Appli
838	296.5	21.6	431	4	US-09-101-272G-1	Sequence 1, Appli	911	276	20.1	306	1	US-08-474-042-1	Sequence 1, Appli
839	296.5	21.6	431	6	518829-1	Patent No. 518829	912	276	20.1	306	1	US-08-484-558-1	Sequence 1, Appli
840	296.5	21.6	431	6	518829-1	Patent No. 518829	913	276	20.1	306	1	US-08-774-592-1	Sequence 1, Appli
841	296.5	21.6	432	2	US-08-560-098A-47	Sequence 47, Appl	914	276	20.1	437	1	US-08-487-037-2	Sequence 2, Appli
842	296	21.5	269	4	US-09-715-994-2	Sequence 2, Appli	915	276	20.1	448	1	US-08-295-411-3	Sequence 3, Appli
843	295.5	21.5	283	3	US-09-478-957-1	Sequence 1, Appli	916	276	20.1	448	2	US-08-955-471-3	Sequence 3, Appli
844	295.5	21.5	283	3	US-09-478-957-1	Sequence 1, Appli	917	276	20.1	448	2	PCT-US92-10068-1	Sequence 1, Appli
845	295.5	21.5	454	3	US-09-518-046-2	Sequence 2, Appli	918	276	20.1	448	5	PCT-US92-10242-3	Sequence 3, Appli
846	294	21.4	256	3	US-09-032-215-32	Sequence 32, Appl	919	276	20.1	488	1	US-08-487-037-1	Sequence 1, Appli
847	293.5	21.4	239	3	US-08-944-483-61	Sequence 61, Appl	920	276	20.1	496	4	US-09-949-016-9524	Sequence 9524, Ap
848	293.5	21.4	411	4	US-09-403-736-2	Sequence 2, Appli	921	274.5	20.0	211	3	US-09-220-731-25	Sequence 25, Appl
849	293.5	21.4	430	1	US-07-942-157A-3	Sequence 3, Appli	922	274.5	20.0	211	4	US-09-242-999-20	Sequence 20, Appl
850	292	21.3	237	3	US-09-004-731-22	Sequence 22, Appl	923	274	19.9	241	1	US-08-330-978-4	Sequence 4, Appli
851	292	21.3	237	3	US-08-749-699-22	Sequence 22, Appl	924	274	19.9	241	1	US-08-474-042-4	Sequence 4, Appli
852	292	21.3	237	4	US-09-004-729-22	Sequence 22, Appl	925	274	19.9	241	1	US-08-484-558-4	Sequence 4, Appli
853	292	21.3	256	3	US-08-906-769-89	Sequence 89, Appl	926	274	19.9	241	1	US-08-774-592-4	Sequence 4, Appli
854	292	21.3	256	3	US-08-906-616-89	Sequence 89, Appl	927	274	19.9	254	1	US-08-330-978-3	Sequence 3, Appli
855	292	21.3	256	3	US-08-817-795-89	Sequence 89, Appl	928	274	19.9	254	1	US-08-474-042-3	Sequence 3, Appli
856	292	21.3	256	3	US-08-639-075A-89	Sequence 89, Appl	929	274	19.9	254	1	US-08-484-558-3	Sequence 3, Appli
857	292	21.3	256	3	US-09-012-431-89	Sequence 89, Appl	930	274	19.9	254	1	US-08-774-592-3	Sequence 3, Appli
858	292	21.3	256	3	US-09-012-692-89	Sequence 89, Appl	931	272	19.8	253	3	US-08-906-769-131	Sequence 131, App
859	292	21.3	256	3	US-08-906-613-89	Sequence 89, Appl	932	272	19.8	253	3	US-08-906-616-131	Sequence 131, App
860	292	21.3	256	5	PCT-US95-14442A-89	Sequence 89, Appl	933	272	19.8	253	3	US-08-639-075A-131	Sequence 131, App
861	292	21.3	414	4	US-09-270-767-46426	Sequence 46426, A	934	272	19.8	253	3	US-09-012-431-131	Sequence 131, App
862	291.5	21.2	242	3	US-08-944-483-57	Sequence 57, Appl	935	272	19.8	253	3	US-09-012-692-131	Sequence 131, App
863	291.5	21.2	253	3	US-08-944-483-73	Sequence 73, Appl	936	272	19.8	253	3	US-08-906-613-131	Sequence 131, App
864	291	21.2	416	2	US-09-000-846-2	Sequence 2, Appli	937	270	19.7	251	3	US-08-944-483-28	Sequence 28, Appl
865	290	21.1	235	2	US-08-557-146-14	Sequence 14, Appl	938	269	19.6	256	4	US-08-395-456C-23	Sequence 23, Appl
866	290	21.1	235	2	US-09-154-344-14	Sequence 14, Appl	939	269	19.6	256	4	US-08-487-453A-23	Sequence 23, Appl
867	290	21.1	235	3	US-08-807-151-3	Sequence 3, Appli	940	268	19.5	256	2	US-08-230-428B-4	Sequence 4, Appli
868	290	21.1	235	3	US-08-944-483-42	Sequence 42, Appl	941	268	19.5	437	1	US-08-487-037-3	Sequence 3, Appli
869	290	21.1	235	3	US-09-478-957-3	Sequence 3, Appli	942	267.5	19.5	266	3	US-09-004-731-24	Sequence 24, Appl
870	289	21.0	223	1	US-07-956-848A-41	Sequence 41, Appl	943	267.5	19.5	266	3	US-08-749-699-24	Sequence 24, Appl
871	289	21.0	223	1	US-08-471-956-41	Sequence 41, Appl	944	267.5	19.5	266	4	US-09-004-729-24	Sequence 24, Appl
872	289	21.0	583	4	US-09-976-594-837	Sequence 837, App	945	265.5	19.3	197	1	US-08-456-840-48	Sequence 48, Appl
873	288.5	21.0	255	3	US-08-906-769-91	Sequence 91, Appl	946	265.5	19.3	197	1	US-08-266-407A-48	Sequence 48, Appl
874	288.5	21.0	255	3	US-08-906-616-91	Sequence 91, Appl	947	265.5	19.3	197	2	US-08-892-544-48	Sequence 48, Appl
875	288.5	21.0	255	3	US-08-817-795-91	Sequence 91, Appl	948	264.5	19.3	248	1	US-08-238-130-2	Sequence 2, Appli
876	288.5	21.0	255	3	US-08-639-075A-91	Sequence 91, Appl	949	264.5	19.3	248	2	US-08-921-426-4	Sequence 4, Appli
877	288.5	21.0	255	3	US-09-012-431-91	Sequence 91, Appl	950	264.5	19.3	248	3	US-08-816-915-4	Sequence 4, Appli
878	288.5	21.0	255	3	US-09-012-692-91	Sequence 91, Appl	951	264.5	19.3	248	5	PCT-US95-07743-4	Sequence 4, Appli
879	288.5	21.0	255	3	US-08-906-613-91	Sequence 91, Appl	952	264.5	19.3	249	3	US-09-578-303-2	Sequence 2, Appli
880	288.5	21.0	255	5	PCT-US95-14442A-91	Sequence 91, Appl	953	264	19.2	250	3	US-08-944-483-68	Sequence 68, Appl
881	288	21.0	268	1	US-08-270-584A-2	Sequence 2, Appli	954	264	19.2	256	4	US-09-949-016-6271	Sequence 6271, Ap
882	288	21.0	268	2	US-08-765-192-2	Sequence 2, Appli	955	263.5	19.2	222	2	US-08-491-204A-18	Sequence 18, Appl
883	288	21.0	268	3	US-09-199-793-2	Sequence 2, Appli	956	263.5	19.2	251	4	US-09-949-016-6112	Sequence 6112, Ap
884	287	20.9	227	3	US-08-944-483-40	Sequence 40, Appl	957	263.5	19.2	255	4	US-09-949-016-9690	Sequence 9690, Ap
885	287	20.9	407	3	US-09-734-675-4	Sequence 4, Appli	958	263	19.1	252	3	US-08-906-769-103	Sequence 103, App
886	286.5	20.9	218	3	US-09-578-303-3	Sequence 3, Appli	959	263	19.1	252	3	US-08-906-616-103	Sequence 103, App
887	286.5	20.9	228	3	US-09-004-731-10	Sequence 10, Appl	960	263	19.1	252	3	US-08-817-795-103	Sequence 103, App
888	286.5	20.9	228	3	US-08-749-699-10	Sequence 10, Appl	961	263	19.1	252	3	US-08-639-075A-103	Sequence 103, App
889	286.5	20.9	228	4	US-09-004-729-10	Sequence 10, Appl	962	263	19.1	252	3	US-09-012-431-103	Sequence 103, App
890	286	20.8	228	4	US-09-205-258-1150	Sequence 1150, Ap	963	263	19.1	252	3	US-08-906-613-103	Sequence 103, App
891	284.5	20.7	225	3	US-09-004-731-13	Sequence 13, Appl	964	263	19.1	252	5	PCT-US95-14442A-103	Sequence 103, App
892	284.5	20.7	225	3	US-08-749-699-13	Sequence 13, Appl	965	263	19.1	252	5	US-09-004-731-27	Sequence 27, Appl
893	284.5	20.7	225	4	US-09-004-729-13	Sequence 13, Appl	966	262.5	19.1	233	3	US-08-906-769-145	Sequence 145, App
894	284.5	20.7	255	3	US-08-906-769-83	Sequence 83, Appl	967	262.5	19.1	233	3	US-08-906-616-145	Sequence 145, App
895	284.5	20.7	255	3	US-08-906-616-83	Sequence 83, Appl	968	262.5	19.1	233	4	US-08-749-699-27	Sequence 27, Appl
896	284.5	20.7	255	3	US-08-817-795-83	Sequence 83, Appl	969	261.5	19.0	222	1	US-07-969-931-9	Sequence 9, Appli
897	284.5	20.7	255	3	US-08-639-075A-83	Sequence 83, Appl	970	261.5	19.0	222	1	US-07-855-417A-9	Sequence 9, Appli
898	284.5	20.7	255	3	US-09-012-431-83	Sequence 83, Appl	971	261.5	19.0	225	3	US-08-944-483-32	Sequence 32, Appl
899	284.5	20.7	255	3	US-09-012-692-83	Sequence 83, Appl	972	257.5	18.7	224	1	US-08-553-516-2	Sequence 2, Appli
900	284.5	20.7	255	3	US-08-906-613-83	Sequence 83, Appl	973	256	18.6	267	3	US-08-906-769-145	Sequence 145, App
901	284.5	20.7	255	5	PCT-US95-14442A-83	Sequence 83, Appl	974	256	18.6	267	3	US-08-906-616-145	Sequence 145, App
902	283.5	20.6	268	3	US-09-032-215-42	Sequence 42, Appl	975	256	18.6	267	3	US-08-639-075A-145	Sequence 145, App
903	282.5	20.6	144	4	US-09-618-259-4	Sequence 4, Appli	976	256	18.6	267	3	US-09-004-731-67	Sequence 67, Appl



977	256	18.6	267	3	US-09-012-431-145	Sequence 145, App	1050	226	16.4	697	3	US-08-462-040-50	Sequence 50, Appl
978	256	18.6	267	3	US-08-749-699-67	Sequence 67, Appl	1051	226	16.4	723	1	US-07-838-410-1	Sequence 1, Appli
979	256	18.6	267	3	US-09-012-692-145	Sequence 145, App	1052	226	16.4	723	1	US-08-290-937B-1	Sequence 1, Appli
980	256	18.6	267	3	US-08-906-613-145	Sequence 145, App	1053	226	16.4	723	1	US-08-290-937B-2	Sequence 2, Appli
981	256	18.6	267	4	US-09-004-729-67	Sequence 67, Appl	1054	226	16.4	723	1	US-08-290-937B-3	Sequence 3, Appli
982	256	18.6	405	3	US-09-734-675-2	Sequence 2, Appli	1055	226	16.4	723	1	US-08-404-643-1	Sequence 1, Appli
983	254	18.5	242	3	US-09-004-731-41	Sequence 41, Appl	1056	226	16.4	723	3	US-09-194-326-1	Sequence 1, Appli
984	254	18.5	242	3	US-08-749-699-41	Sequence 41, Appl	1057	226	16.4	723	3	US-09-194-326-2	Sequence 2, Appli
985	254	18.5	242	4	US-09-004-729-41	Sequence 41, Appl	1058	226	16.4	723	3	US-09-194-326-3	Sequence 3, Appli
986	254	18.5	255	4	US-09-270-767-44361	Sequence 44361, A	1059	226	16.4	723	3	US-08-700-519J-19	Sequence 19, Appl
987	253	18.4	182	4	US-09-328-925-12	Sequence 12, Appl	1060	226	16.4	723	4	US-09-600-991-18	Sequence 18, Appl
988	253	18.4	231	4	US-08-395-456C-25	Sequence 25, Appl	1061	226	16.4	723	4	US-08-605-221-4	Sequence 4, Appli
989	253	18.4	242	3	US-09-032-215-47	Sequence 47, Appl	1062	226	16.4	723	4	US-08-605-221-2	Sequence 2, Appli
990	252.5	18.4	221	2	US-08-925-708-1	Sequence 1, Appli	1063	226	16.4	723	4	US-09-601-040A-10	Sequence 10, Appl
991	252.5	18.4	239	3	US-09-004-731-44	Sequence 44, Appl	1064	226	16.4	728	1	US-07-815-333A-2	Sequence 2, Appli
992	252.5	18.4	239	3	US-08-749-699-44	Sequence 44, Appl	1065	226	16.4	728	1	US-08-087-783A-22	Sequence 22, Appl
993	252.5	18.4	239	4	US-09-004-729-44	Sequence 44, Appl	1066	226	16.4	728	4	US-08-605-221-2	Sequence 2, Appli
994	252.5	18.4	247	3	US-08-944-483-49	Sequence 49, Appl	1067	222	16.2	723	3	US-08-030-410-3	Sequence 3, Appli
995	252	18.3	229	4	US-08-395-456C-27	Sequence 27, Appl	1068	222	16.2	213	3	US-08-906-769-149	Sequence 149, App
996	251	18.3	229	2	US-08-394-600B-20	Sequence 20, Appl	1069	222	16.2	213	3	US-08-906-616-149	Sequence 149, App
997	251	18.3	229	4	US-08-395-456C-20	Sequence 20, Appl	1070	222	16.2	213	3	US-08-639-075A-149	Sequence 149, App
998	251	18.3	229	4	US-08-487-453A-20	Sequence 20, Appl	1071	222	16.2	213	3	US-09-012-431-149	Sequence 149, App
999	251	18.3	229	5	PCT-US95-02513-20	Sequence 20, Appl	1072	222	16.2	213	3	US-09-012-692-149	Sequence 149, App
1000	250	18.2	352	4	US-09-902-540-9796	Sequence 9796, Ap	1073	222	16.2	234	3	US-08-906-613-149	Sequence 149, App
1001	248.5	18.1	717	4	US-09-601-040A-6	Sequence 6, Appli	1074	220.5	16.0	267	2	US-08-944-483-56	Sequence 56, Appl
1002	248.5	18.1	729	4	US-09-601-040A-2	Sequence 2, Appli	1075	220	16.0	278	4	US-08-978-404B-46	Sequence 46, Appl
1003	247.5	18.0	717	4	US-09-601-040A-8	Sequence 8, Appli	1076	220	16.0	457	4	US-09-270-767-48024	Sequence 48024, A
1004	247.5	18.0	729	4	US-09-601-040A-4	Sequence 4, Appli	1077	217.5	15.8	457	4	US-09-270-767-32807	Sequence 32807, A
1005	247	18.0	229	3	US-08-944-483-30	Sequence 30, Appl	1078	217.5	15.8	385	4	US-09-163-951-16	Sequence 16, Appl
1006	245	17.8	226	4	US-09-601-040A-28	Sequence 28, Appl	1079	216	15.7	385	4	US-09-345-881-16	Sequence 16, Appl
1007	245	17.8	228	2	US-08-766-982-11	Sequence 11, Appl	1080	216	15.7	185	3	US-08-906-769-141	Sequence 141, App
1008	245	17.8	228	3	US-08-944-483-55	Sequence 55, Appl	1081	216	15.7	185	3	US-08-906-616-141	Sequence 141, App
1009	245	17.8	228	3	US-09-296-219-11	Sequence 11, Appl	1082	216	15.7	185	3	US-08-639-075A-141	Sequence 141, App
1010	245	17.8	711	1	US-08-184-012C-8	Sequence 8, Appli	1083	216	15.7	185	3	US-09-012-431-141	Sequence 141, App
1011	245	17.8	711	1	US-08-334-177-2	Sequence 2, Appli	1084	216	15.7	185	3	US-09-012-692-141	Sequence 141, App
1012	245	17.8	711	2	US-08-666-082B-1	Sequence 1, Appli	1085	216	15.7	223	1	US-08-906-613-141	Sequence 141, App
1013	245	17.8	711	2	US-08-766-982-2	Sequence 2, Appli	1086	216	15.7	223	1	US-08-278-091-13	Sequence 13, Appl
1014	245	17.8	711	3	US-09-296-219-2	Sequence 2, Appli	1087	216	15.7	223	1	US-08-483-859-13	Sequence 13, Appl
1015	245	17.8	711	4	US-09-600-991-20	Sequence 20, Appl	1088	216	15.7	223	1	US-08-472-173-13	Sequence 13, Appl
1016	245	17.8	711	4	US-09-601-040A-12	Sequence 12, Appl	1089	216	15.7	223	2	US-08-487-167-13	Sequence 13, Appl
1017	245	17.8	711	4	US-09-949-016-6981	Sequence 12, Appl	1090	216	15.7	223	2	US-08-482-816-13	Sequence 13, Appl
1018	245	17.8	711	5	PCT-US95-13830-2	Sequence 6981, Ap	1091	216	15.7	223	2	US-08-296-149-13	Sequence 13, Appl
1019	244.5	17.8	716	2	US-08-766-982-1	Sequence 2, Appli	1092	216	15.7	223	2	US-08-801-499-13	Sequence 13, Appl
1020	244.5	17.8	716	3	US-09-296-219-1	Sequence 1, Appli	1093	216	15.7	223	2	US-08-615-271-13	Sequence 13, Appl
1021	242	17.6	214	6	5180819-3	Sequence 1, Appli	1094	216	15.7	223	3	US-09-074-660-13	Sequence 13, Appl
1022	242	17.6	214	6	5180819-3	Patent No. 5180819	1095	216	15.7	223	3	US-09-074-659-13	Sequence 13, Appl
1023	242	17.6	455	3	US-09-261-416-2	Patent No. 5180819	1096	216	15.7	223	3	US-09-106-468-13	Sequence 13, Appl
1024	240	17.5	161	3	US-09-261-416-8	Sequence 2, Appli	1097	216	15.7	223	3	US-09-106-466A-13	Sequence 13, Appl
1025	234	17.0	158	3	US-09-518-046-22	Sequence 8, Appli	1098	211	15.7	223	3	US-09-106-467-13	Sequence 13, Appl
1026	232.5	16.9	185	3	US-08-705-875A-5	Sequence 22, Appl	1099	211	15.4	223	1	US-08-485-455D-17	Sequence 17, Appl
1027	232.5	16.9	185	3	US-09-220-731-22	Sequence 5, Appli	1099	211	15.4	223	2	US-08-485-455D-17	Sequence 17, Appl
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1029	231.5	16.8	219	2	US-08-925-708-2	Sequence 5, Appli	1101	211	15.4	223	2	US-08-484-211C-17	Sequence 17, Appl
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1387 104.5 7.6 441 4 US-09-949-016-10792 Sequence 10792, A  
1388 102.5 7.5 80 1 US-08-485-455D-59 Sequence 59, Appl  
1389 102.5 7.5 80 2 US-08-482-130C-59 Sequence 59, Appl  
1390 102.5 7.5 80 2 US-08-484-211C-59 Sequence 59, Appl  
1391 102.5 7.5 80 3 US-08-906-769-59 Sequence 59, Appl  
1392 102.5 7.5 80 3 US-08-906-616-59 Sequence 59, Appl  
1393 102.5 7.5 80 3 US-08-817-795-59 Sequence 59, Appl  
1394 102.5 7.5 80 3 US-08-485-443B-59 Sequence 59, Appl  
1395 102.5 7.5 80 3 US-08-639-075A-59 Sequence 59, Appl  
1396 102.5 7.5 80 3 US-09-012-431-59 Sequence 59, Appl  
1397 102.5 7.5 80 3 US-09-012-692-59 Sequence 59, Appl  
1398 102.5 7.5 80 3 US-08-906-613-59 Sequence 59, Appl  
1399 102.5 7.5 80 5 PCT-US95-14442A-59 Sequence 59, Appl  
1400 101.5 7.4 117 4 US-09-270-767-32317 Sequence 32317, A  
1401 101.5 7.4 117 4 US-09-270-767-47534 Sequence 47534, A  
1402 101 7.4 125 4 US-09-270-767-33002 Sequence 33002, A  
1403 101 7.4 125 4 US-09-270-767-48219 Sequence 48219, A  
1404 101 7.4 339 4 US-09-543-681A-6965 Sequence 6965, Ap  
1405 100.5 7.3 55 4 US-08-843-076D-22 Sequence 22, Appl  
1406 100 7.3 68 1 US-08-485-455D-77 Sequence 77, Appl  
1407 100 7.3 68 2 US-08-482-130C-77 Sequence 77, Appl  
1408 100 7.3 68 2 US-08-484-211C-77 Sequence 77, Appl  
1409 100 7.3 68 3 US-08-906-769-77 Sequence 77, Appl  
1410 100 7.3 68 3 US-08-906-616-77 Sequence 77, Appl  
1411 100 7.3 68 3 US-08-817-795-77 Sequence 77, Appl  
1412 100 7.3 68 3 US-08-485-443B-77 Sequence 77, Appl  
1413 100 7.3 68 3 US-08-639-075A-77 Sequence 77, Appl  
1414 100 7.3 68 3 US-09-012-431-77 Sequence 77, Appl





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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6948
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6948

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RESULT 3  
 US-09-244-111-6  
 ; Sequence 6, Application US/09244111  
 ; Patent No. 6566498  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni, et al.  
 ; TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides  
 ; FILE REFERENCE: PF391  
 ; CURRENT APPLICATION NUMBER: US/09/244,111  
 ; CURRENT FILING DATE: 1999-02-04  
 ; EARLIER APPLICATION NUMBER: 60/073,961  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 162  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-244-111-6

QY	121	TSSVQPLPLPNDCA	TAGTECHVSGWG	ITNHP	PNPFDLLQCLNLS	IVSHAT	CHGVYP	PGRI	180
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Db	70	-----	-----	-----	-----	-----	-----	-----	94
					PDLLQCLNLS	IVSHAT	CHGVYP	PGRI	
QY	181	TSNMVCAGGVP	GDACQD	SGGPLVCGGV	LQGLVSWG	SVGPCGD	GIPGV	VTYICKY	VDW
Db	95	TSNMVCAGGVP	GDACQD	SGGPLVCGGV	LQGLVSWG	SVGPCGD	GIPGV	VTYICKY	VDW
QY	241	IRMIMRNN							248
Db	155	IRMIMRNN							162

RESULT 4  
 US-09-618-259-7  
 ; Sequence 7, Application US/09618259  
 ; Patent No. 6642013  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'Brien, Timothy J.  
 ; APPLICANT: Underwood, Lowell J.  
 ; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
 ; FILE REFERENCE: D6020CIP2  
 ; CURRENT APPLICATION NUMBER: US/09/618,259  
 ; CURRENT FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: US 09/127,444  
 ; PRIOR FILING DATE: 1998-08-21  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SEQ ID NO 7  
 ; LENGTH: 260  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Amino acid sequence of TADG-14 protein  
 US-09-618-259-7

RESULT 5  
US-09-070-526-2  
; Sequence 2, Application US/09070526  
; Patent No. 6100059  
; GENERAL INFORMATION:  
; APPLICANT: SOUTHAN, CHRISTOPHER  
; APPLICANT: CLINKENBEARD, HELEN  
; APPLICANT: BURGESS, NICOLA  
; TITLE OF INVENTION: No. 6100059el Compounds  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980

;  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,526  
; FILING DATE: 30-APR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9711952.3  
; FILING DATE: 9-JUN-1997  
; APPLICATION NUMBER: EP 97309646.4  
; FILING DATE: 1-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-30353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
;  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 260 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
;  
US-09-070-526-2

Query Match 45.6%; Score 626.5; DB 3; Length 260;  
Best Local Similarity 50.4%; Pred. No. 6.2e-53;  
Matches 122; Conservative 23; Mismatches 92; Indels 5; Gaps 3;  
  
QY 5 IFLL--CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61  
Db 13 MFLLLGGAWAGHSAQEDKVLGHECQPHSQPWQAALFQGGQLLCGGVLVGNWVLTAA 72  
  
QY 62 HCSGSRYWVRLGEHSLSDWTEQIRHSGFSVTHPGYLCAST-SHEHDLRLRLPVRV 120  
Db 73 HCKPKYTVRLGDHSLQNKDGPQEIPVQSIHPFCYNSSDVEDHNDMLLQLRDQASL 132  
  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNFPDQLLQCLNLSIVSHATCHGVYPGR 180  
Db 133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQ 192  
  
QY 181 TSNMVCAGVPGQACQDGGPLVCGGVLPGLVSGSVGPCGQDGIPIGVVYTYICKYVDW 240  
Db 193 TDGMVCAGSSKGADTCQDGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW 251  
  
QY 241 IR 242  
Db 252 IK 253

RESULT 6  
US-09-025-059-3  
; Sequence 3, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.

;  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
;  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
;  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 260 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1020091  
;  
US-09-025-059-3

Query Match 45.3%; Score 622.5; DB 3; Length 260;  
Best Local Similarity 49.0%; Pred. No. 1.5e-52;  
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;  
  
QY 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61  
Db 13 ILLLLFMGAWAGLTRAQGSKILEGRECIHPHQWQAALFQGERLICGGVLVGRWVLTAA 72  
  
QY 62 HCSGSRYWVRLGEHSLSDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLPVRV 120  
Db 73 HCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPFCYNNNSNPEDHSHDMLRLQNSANL 132  
  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNFPDQLLQCLNLSIVSHATCHGVYPGR 180  
Db 133 GDKVKPVQLANLCPKVQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQKNCERAYPGKI 192  
  
QY 181 TSNMVCAGVPGQACQDGGPLVCGGVLPGLVSGSVGPCGQDGIPIGVVYTYICKYVDW 240  
Db 193 TEGMVCAGSSNGADTCQDGGPLVCDGMLQGITSWGS-DPCGKPEKPGVYTKICRYTTW 251  
  
QY 241 IRMIMRN 247  
Db 252 IKKTMND 258

RESULT 7  
US-09-008-271A-7  
; Sequence 7, Application US/09008271A  
; Patent No. 6203979  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES



; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNOT27
; CLONE: 1798496
; SEQUENCE DESCRIPTION: SEQ ID NO: 7 :
US-09-008-271A-7

Query Match 45.3%; Score 622.5; DB 3; Length 260;
Best Local Similarity 49.8%; Pred. No. 1.5e-52;
Matches 122; Conservative 24; Mismatches 94; Indels 5; Gaps 3;
QY 5 IFLL--CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
Db 13 MFLLLGGAWAGHRAQEDKVLGHECQPHSQPWQAALSQGGQLCGVLVGNWVLTAA 72
QY 62 HCSGSRYWVRLGEHSLSQLDWTQEIIRHSGFVTHPGYLGAST-SHEHDLRLRLPVRV 120
Db 73 HCKKPKYTVRLGHSIQNKDGPQEIPVVQSIHPHCYNSSDVEDHNDLMLQLRDQASL 132
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQLCLNLSIVSHATCHGVYPGRI 180
Db 133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
QY 181 TSNMVCAGGVPQDACQDGGPLVCGGLVQGLVSWGSGVPCGQDGIPIGVYTYICKYVDW 240
Db 193 TDGMVCAGSSKGADTCQDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLDW 251
QY 241 IRMIM 245
Db 252 IKKII 256

RESULT 8
US-09-618-259-8
; Sequence 8, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259

; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 8
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous
; OTHER INFORMATION: to TADG-14; accession no. D30785
US-09-618-259-8
Query Match 45.3%; Score 622.5; DB 4; Length 260;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;
QY 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
Db 13 ILLLLFMGAWAGLTRAQGSKILEGRECIPIHSPQWQAALFOGERLICGGVLVGDWRVLTAA 72
QY 62 HCSGSRYWVRLGEHSLSQLDWTQEIIRHSGFVTHPGYLGAS-TSHEHDLRLRLPVRV 120
Db 73 HCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSPEDHSHDMLRLQNSANL 132
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQLCLNLSIVSHATCHGVYPGRI 180
Db 133 GDKVKPVQLANLCPKVGQKCIISGWTGTVTSPEQENFNTLNCAEVKIYSONKCEPAYPGKI 192
QY 181 TSNMVCAGGVPQDACQDGGPLVCGGLVQGLVSWGSGVPCGQDGIPIGVYTYICKYVDW 240
Db 193 TEGMVCAGSSNGADTCQDGGPLVCDGMLQGITSWGSDPCGKPEKPGVYTKICRYTTW 251
QY 241 IRMIMRN 247
Db 252 IKKTMND 258

RESULT 9
US-09-205-258-427
; Sequence 427, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 427  
LENGTH: 250  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-427

Query Match 45.0%; Score 618.5; DB 4; Length 250;  
Best Local Similarity 48.2%; Pred. No. 3.5e-52;  
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;  
QY 3 LSIFLLLCVLGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62  
Db 4 LQILLLALATGLVGGET-RIKGFCKPHSQPQAALFEKTRLLCGATLIAPRWLLTAAH 62  
QY 63 CSGSRVWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGA--STSHEHDLRLRLPVRV 120

Db 63 CLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPCFNNSLPNKDHRNDIMLVKNASPVSI 122  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNRPFPDQLLQCLNLSIVSHATCHGVYPGRI 180  
Db 123 TWAVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIHQKCNAYPGNI 182  
QY 181 TSNMVCAG-GVPQDACQDGGPLVCGGVLQGLVSWGSVGPCCQDGIPIGVVTVICKYVD 239  
Db 183 TDTMVCASVQEGKDSQCQDGGPLVCNQLQGIISWGQ-DPCAITRKPGVYTKVCKYVD 241  
QY 240 WIRMIMRNN 248  
Db 242 WIQETMKN 250  
RESULT 10  
US-09-025-059-1  
; Sequence 1, Application US/09025059  
; Patent No. 6075136  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,059  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0481 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 282 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGTUT10  
; CLONE: 2723646  
; US-09-025-059-1

Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 4.1e-52;  
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;  
QY 3 LSIFLLLCVLGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62  
Db 36 LQILLLALATGLVGGET-RIKGFCKPHSQPQAALFEKTRLLCGATLIAPRWLLTAAH 94  
QY 63 CSGSRVWVRLGHSLSQLDWTQIRHSGFSVTHPGYLGA--STSHEHDLRLRLPVRV 120

Db 95 CLKPRYIVHLGQHNQKEEGCEQTRTATESPPHPGFNNSLPNKDHNRNDIMLVKMASPVSI 154  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRNPFDPDLLQCLNLSIVSHATCHGVYPGRI 180  
Db 155 TWAVRPLTLSSRCVTAGTSCLSISGWGSTSSPOLRLPHTLRCANITIEHQKCNAYPGNI 214  
QY 181 TSNMVCAG-GVPGQDACQDSDGGPLVCGGVLCGLVSWGSGVPGCGQDGIPGVYTYICKYVD 239  
Db 215 TDTMVCASVQEGKXSCQDSDGGPLVCNQSLOGLIISWGQ-DPCAITRKPGVYTKVCKYVD 273  
QY 240 WIRMIMRNN 248  
Db 274 WIQETMKN 282

RESULT 11  
US-09-386-642-13  
; Sequence 13, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-13

Query Match 43.9%; Score 602.5; DB 4; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.5e-50;  
Matches 116; Conservative 21; Mismatches 87; Indels 3; Gaps 3;  
QY 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRVWVRLGEHLSQ 79  
Db 51 KIVGGYNCLEPHSQPWQAALFQGGQLCGVLVGGNWLTAHCKPKYTVRLGDHSLQ 110  
QY 80 LDWTEQIRHSGFSVTHPGYLGA-STSHEDLRLRLPVRVTSSVQPLPNDCATAGT 138  
Db 111 KDGEQEIIPVQSIHPHCYNSSDVEDHNHDLMLQLRDQASLGSKVKPISLADHCTPGQ 170  
QY 139 ECHVSGWGITNHRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQDACQ 198  
Db 171 KCTVSGWGTVTSRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGSSKGADTCQ 230  
QY 199 DSGGPLVCGVLQGLVSWGSGVPGCGQDGIPGVYTYICKYVDWIRMIM 245  
Db 231 DSGGPLVCDGALQGITSWGSD-PCGGRSDKPGVYTNICRYLDWIKKII 276

RESULT 12  
US-09-386-642-14  
; Sequence 14, Application US/09386642  
; Patent No. 6420157  
; GENERAL INFORMATION:  
; APPLICANT: Darrow, Andrew  
; APPLICANT: Qi, Jensen  
; APPLICANT: Andrade-Gordon, Patricia  
; TITLE OF INVENTION: Zymogen Activation System  
; FILE REFERENCE: ORT-1028  
; CURRENT APPLICATION NUMBER: US/09/386,642  
; CURRENT FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14  
; LENGTH: 289  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene  
; OTHER INFORMATION: with homo sapien serine protease catalytic domain  
US-09-386-642-14  
Query Match 43.6%; Score 598.5; DB 4; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.8e-50;  
Matches 114; Conservative 34; Mismatches 79; Indels 5; Gaps 4;  
QY 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRVWVRLGEHLSQ 79  
Db 51 KIVGGYNCLEKHSQPWQAALFEKTRLLCGATLIAPRWLLTAHCLKPRYIVHLGQHNLOK 110  
QY 80 LDWTEQIRHSGFSVTHPGYLGA-STSHEDLRLRLPVRVTSSVQPLPNDCATAG 137  
Db 111 EEGCEQTRTATESFPHPGFNNSLPNKDHNRNDIMLVKMASPVSIWAVRPLTLSSRCVTAG 170  
QY 138 TECHVSGWGITNHRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAG-GVPGQDAC 196  
Db 171 TSCLISGWGSTSSPOLRLPHTLRCANITIEHQKCNAYPGNITDGMVCASVQEGKXSC 230  
QY 197 QGDSGGPLVCGVLQGLVSWGSGVPGCGQDGIPGVYTYICKYVDWIRMIMRNN 248  
Db 231 QGDSGGPLVCNQSLOGLIISWGQ-DPCAITRKPGVYTKVCKYVDWIQETMKN 281

RESULT 13  
US-08-944-483-24  
; Sequence 24, Application US/08944483  
; Patent No. 6232456  
; GENERAL INFORMATION:  
; APPLICANT: COHEN, MAURICE  
; APPLICANT: COLPITTS, TRACEY L.  
; APPLICANT: FRIEDMAN, PAULA N.  
; APPLICANT: GRANADOS, EDWARD N.  
; APPLICANT: KLASS, MICHAEL R.  
; APPLICANT: RUSSELL, JOHN C.  
; APPLICANT: STEWART, KENT D.  
; APPLICANT: STROUPE, STEVEN D.  
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS  
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES  
; TITLE OF INVENTION: OF THE PROSTATE  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,483  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 6183.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623



```
;
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-24

Query Match          43.5%; Score 597.5; DB 3; Length 248;
Best Local Similarity 47.8%; Pred. No. 3.9e-50;
Matches 119; Conservative 36; Mismatches 87; Indels 7; Gaps 6;

QY 3 LSIFLLLCVLGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 4 LQLILLALATGLVCGET-RIIKGFEC-PHSQPWQAALFK-TRLLCGATLIAPRWLLTAAH 60
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 63 CSGSRYWVRLGEHSLSQLDWTETQIRHSGFSVTHPGYLGA--STSHEHDLRLRLPVRV 120
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 61 CLKPRYIVHLGQHNLKQEEGCEQTRTATESFPHPGFNNSLPNKDHNRDIMLVKMASPVSI 120
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFPPDLLQCLNLSIVSHATCHGVYPGRI 180
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 121 TWAVRPLTLSSRCVTAGTSLISGWGSTSSPQLRPLPHTLRLCANITIIHQKCNAYPGNI 180
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 181 TSNMVCAG-GVPGDACQGDGGPLVCGGVQLGLVSWGSGVGPCGQDGIPGVYTYICKYVD 239
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |
Db 181 TDTMVCASVQEGGKDSQGDGGPLVCNQLQGIISWGQ-DPCAITRKPGVYTKVCKYVD 239
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |

QY 240 WIRMIMRNN 248
   | : | : | | |
Db 240 WIQETMKNN 248
   | : | : | | |

RESULT 14
US-08-956-267A-2
; Sequence 2, Application US/08956267A
; Patent No. 5945328
; GENERAL INFORMATION:
; APPLICANT: WOLDIKE, Helle Fabricius
; APPLICANT: KJELDSSEN, Thomas Borglum
; TITLE OF INVENTION: A Process For Producing Trypsin
; TITLE OF INVENTION: (Trypsinogen)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5945328o No. 5945328disk of No. 5945328th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,267A
; FILING DATE: 22-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rozek, Carol
; REGISTRATION NUMBER: 36,993
; REFERENCE/DOCKET NUMBER: 4500.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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;
; MOLECULE TYPE: protein
US-08-956-267A-2

Query Match          41.7%; Score 573; DB 2; Length 247;
Best Local Similarity 45.6%; Pred. No. 9.3e-48;
Matches 113; Conservative 42; Mismatches 83; Indels 10; Gaps 5;

QY 6 FLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 5 FVLLALLGAAVAFPTDDDDKIVGGYTCAANSIPYQVSLNSGSHF-CGGSLLNSQWVVVSA 63
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 62 HCSGSRYWVRLGEHSLSQLDWTETQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVT 121
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 64 HCYKSRIQVRLGEHNIDVLENEQFINAAKIIITHPNFNG--NTLDNDIMLIKLSPPATLN 121
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 122 SSVQPLPLPNDCATAGTECHVSGWGITNHPNPFPPDLLQCLNLSIVSHATCHGVYPGRIT 181
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 122 SRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSSLQCLKAPVLSDSCKSSYPGQIT 181
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 182 SNMVCAGGVP-QDACQGDGGPLVCGGVQLGLVSWGSGVGPCGQDGIPGVYTYICKYVDW 240
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |
Db 182 GNMICVGFLEGGKDSQGDGGPVVVCNGLOQIVSWGY--GCAQKNKPGVYTKVCNYYNW 239
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |

QY 241 IRMIMRNN 248
   | : | : | | |
Db 240 IQQTIAAN 247
   | : | : | | |

RESULT 15
US-09-949-016-8166
; Sequence 8166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8166
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8166

Query Match          41.3%; Score 567; DB 4; Length 290;
Best Local Similarity 46.8%; Pred. No. 4.4e-47;
Matches 116; Conservative 36; Mismatches 80; Indels 16; Gaps 6;

QY 13 GLSQAATPKIFN-----GTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 31 GVSQESS-KVLNTNGTSGFLPGGYTCFPHSQPWAALLVQGRLLCGVLVHPKMWLTAAH 89
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 63 CSGSRYWVRLGEHSLSQLDWTETQIRHSGFSVTHPGYLGA--SHEHDLRLRLPVRV 120
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 90 CLKEGLKVYLGHKHALGRVEAGEQVRVVHSHIPPEYRRSPHTLNDHNDIMLLELQSPVOL 149
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 121 TSSVQPLPLP-NDCATAGTECHVSGWGITNHPNPFPPDLLQCLNLSIVSHATCHGVYPGR 179
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |
Db 150 TGYIQTLPPLSHNNRLTPGTTCTRVSGWGTTTSPQVNYPKTLQCANIQLRSDEECRQVYPGK 209
   | : | | | | | : | : | | | | : | | | | | | | | | | | | | | | |

QY 180 ITSNMVCAGGVP-QDACQGDGGPLVCGGVQLGLVSWGSGVGPCGQDGIPGVYTYICKYV 238
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |
Db 210 ITDNMLCAGTKEGGKDSCEGDSGGPLVCNRTLGIIVSWGDF-PCGQPDPRPGVYTRVSRV 268
   | : | | | | | : | : | | | | | | | | | | | | | | | | | | | |
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QY 239 DWIRMINR 246  
||| :|  
Db 269 LWIRETIR 276

Search completed: March 5, 2005, 17:58:17  
Job time : 52 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2005, 17:40:31 ; Search time 133 Seconds  
(without alignments)  
613.557 Million cell updates/sec

Perfect score: 1374  
Sequence: 1 MGLSIFLLCLVLGLSQAATP.....GVYTYICKYVDWIRMNRNN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTU5\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB ID	Description
	Score	Match	Length		
37	1374	100.0	248	14 US-10-013-909A-194	Sequence 194, App
65	1374	100.0	248	15 US-10-344-394-31	Sequence 31, Appl
68	1367	99.5	248	14 US-10-290-058A-12	Sequence 12, Appl
69	811	59.0	162	14 US-10-325-745-6	Sequence 6, Appli
70	630.5	45.9	260	9 US-09-796-294-7	Sequence 7, Appli
121	630.5	45.9	260	14 US-10-167-749-395	Sequence 395, App
246	630.5	45.9	260	14 US-10-223-085-72	Sequence 72, Appl
250	630.5	45.9	260	14 US-10-223-084-72	Sequence 72, Appl
251	630.5	45.9	260	14 US-10-223-088-72	Sequence 72, Appl
252	630.5	45.9	260	14 US-10-223-090-72	Sequence 72, Appl
253	630.5	45.9	260	14 US-10-223-087-72	Sequence 72, Appl
255	630.5	45.9	260	14 US-10-223-083-72	Sequence 72, Appl
256	630.5	45.9	260	14 US-10-223-089-72	Sequence 72, Appl
426	630.5	45.9	260	14 US-10-223-081-72	Sequence 72, Appl



1295	564.5	41.1	293	10	US-09-997-428-309	Sequence 309, App
1340	564.5	41.1	293	11	US-09-938-671-82	Sequence 82, Appl
1341	564.5	41.1	293	11	US-09-938-671-97	Sequence 97, Appl

Search completed: March 5, 2005, 17:57:36  
Job time : 150 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 5, 2005, 17:48:47 ; Search time 40 Seconds  
(without alignments)  
596.544 Million cell updates/sec

Title: US-10-006-856A-194  
Perfect score: 1374  
Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVVITYICKYVDWIRMNRNN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : PIR\_79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622.5	45.3	260	2 I56559	neuropsin - mouse
2	569.5	41.4	248	2 S55066	trypsin (EC 3.4.21
3	567	41.3	248	2 S55067	trypsin (EC 3.4.21
4	561	40.8	231	1 TRPGTR	trypsin (EC 3.4.21
5	555	40.4	243	2 A35871	trypsin (EC 3.4.21
6	555	40.4	253	2 A53968	serine proteinase
7	553	40.2	246	2 B25528	trypsin (EC 3.4.21
8	552	40.2	229	1 TRBOTR	trypsin (EC 3.4.21
9	550	40.0	247	2 S13813	trypsin (EC 3.4.21
10	546	39.7	247	1 TRDG	trypsin (EC 3.4.21
11	545	39.7	246	1 TRDGC	trypsin (EC 3.4.21
12	544.5	39.6	247	2 A27547	trypsin (EC 3.4.21
13	543	39.5	246	1 TRRT1	trypsin (EC 3.4.21
14	540	39.3	238	2 S31779	trypsin (EC 3.4.21
15	533.5	38.8	247	2 S05494	trypsin (EC 3.4.21
16	532	38.7	246	1 TRRT2	trypsin (EC 3.4.21
17	527.5	38.4	261	2 A31136	tissue kallikrein
18	524	38.1	232	1 KQPG	tissue kallikrein
19	520.5	37.9	261	2 A25606	tissue kallikrein
20	519	37.8	246	2 JQ1471	trypsin (EC 3.4.21
21	518	37.7	246	2 JQ1472	trypsin (EC 3.4.21
22	518	37.7	261	2 A34079	tissue kallikrein
23	513.5	37.4	231	2 S31778	trypsin (EC 3.4.21
24	513.5	37.4	239	2 A27207	tissue kallikrein
25	511.5	37.2	261	2 S45303	tissue kallikrein
26	510.5	37.2	261	1 NGMSG	7S nerve growth fa
27	508	37.0	242	2 S31776	trypsin (EC 3.4.21
28	508	37.0	242	2 S31775	trypsin (EC 3.4.21
29	503	36.6	260	2 A37938	tissue kallikrein

30	503	36.6	263	2	S15686	tissue kallikrein
31	502	36.5	259	2	B31136	tissue kallikrein
32	501	36.5	247	1	B25852	trypsin (EC 3.4.21
33	499.5	36.4	241	2	S39048	trypsin (EC 3.4.21
34	496.5	36.1	261	1	TRMSM5	tissue kallikrein
35	496	36.1	242	2	S49489	trypsin (EC 3.4.21
36	495.5	36.1	257	2	S33772	tissue kallikrein
37	495.5	36.1	261	2	S01971	tissue kallikrein
38	494.5	36.0	247	1	A25852	trypsin (EC 3.4.21
39	493	35.9	262	1	KQHU	tissue kallikrein
40	491.5	35.8	240	2	S39047	trypsin (EC 3.4.21
41	491	35.7	256	1	NGMSA	7S nerve growth fa
42	490.5	35.7	229	1	TRDFS	trypsin (EC 3.4.21
43	490.5	35.7	261	2	A41020	tissue kallikrein
44	489	35.6	244	2	A44284	tissue kallikrein
45	485.5	35.3	261	2	JE0236	tissue kallikrein
46	484.5	35.3	259	2	A29746	tissue kallikrein
47	484.5	35.3	304	2	S33496	trypsin (EC 3.4.21
48	483.5	35.2	265	1	KQRTF	tissue kallikrein
49	481.5	35.0	250	2	T01779	trypsin (EC 3.4.21
50	481.5	35.0	261	2	A29745	tissue kallikrein
51	479	34.9	261	1	S35711	semenogelase (EC 3
52	477.5	34.8	261	1	KQMS1	tissue kallikrein
53	476	34.6	259	2	I38363	trypsin (EC 3.4.21
54	470.5	34.2	261	1	A32297	semenogelase (EC 3
55	469.5	34.2	261	2	A24378	tissue kallikrein
56	468	34.1	259	1	KQRTTN	tonin (EC 3.4.21.-
57	467.5	34.0	261	1	EGMSB	tissue kallikrein
58	467	34.0	247	2	S12764	trypsin (EC 3.4.21
59	461.5	33.6	259	2	D23863	tissue kallikrein
60	458.5	33.4	250	2	S31384	trypsin (EC 3.4.21
61	458.5	33.4	261	2	A29586	tissue kallikrein
62	449	32.7	258	2	A57290	venom plasminogen
63	436.5	31.8	250	2	S15685	kallikrein, glandu
64	436.5	31.8	257	1	JC2479	venombin B (EC 3.4
65	432	31.4	236	1	A32121	snake venom factor
66	431.5	31.4	261	2	A28062	gamma-renin (EC 3.
67	431	31.4	262	1	JC4803	venombin A (EC 3.4
68	422.5	30.7	233	1	JG0169	venombin A (EC 3.4
69	417	30.3	236	1	B32121	snake venom factor
70	411.5	29.9	228	1	S35689	venombin A (EC 3.4
71	408	29.7	235	1	S65621	venombin AB (EC 3.
72	406.5	29.6	231	2	A60468	venombin A (EC 3.4
73	402	29.3	255	1	A28169	venombin A (EC 3.4
74	394	28.7	236	1	A41456	pancreatic elastas
75	388	28.2	269	2	A26823	venombin A (EC 3.4
76	386	28.1	232	1	A54361	venombin A (EC 3.4
77	385.5	28.1	188	2	B32340	tissue kallikrein
78	385.5	28.1	264	2	I38136	chymotrypsin-like
79	382.5	27.8	1524	2	T30337	polypotein - Afri
80	382	27.8	246	1	DBHU	complement factor
81	381	27.7	263	1	I55608	complement factor
82	377	27.4	225	2	S45356	probable serine pr
83	374.5	27.3	259	1	WMMS28	complement factor
84	371	27.0	271	1	ELRT2	pancreatic elastas
85	370.5	27.0	263	2	A21195	chymotrypsin (EC 3
86	370	26.9	234	1	S20407	venombin A (EC 3.4
87	368.5	26.8	343	1	A57014	proctasin (EC 3.4.
88	367.5	26.7	638	1	KQHUP	plasma kallikrein
89	366	26.6	258	1	S36783	venombin A (EC 3.4
90	364	26.5	156	2	B23863	tissue kallikrein
91	362.5	26.4	246	2	S64707	chymase (EC 3.4.21
92	359.5	26.2	277	2	S35340	trypsin (EC 3.4.21
93	359	26.1	443	2	I46932	coagulation factor
94	358	26.1	812	1	PLBO	plasmin (EC 3.4.21
95	357	26.0	262	1	A31372	granzyme A (EC 3.4
96	357	26.0	263	2	A31299	chymotrypsin (EC 3
97	357	26.0	271	2	S29239	chymotrypsin (EC 3
98	357	26.0	1019	2	A38738	coagulation factor
99	355.5	25.9	276	2	A38654	mast cell proteina
100	354	25.8	271	2	A25528	pancreatic elastas
101	353.5	25.7	263	2	S47537	chymotrypsin (EC 3
102	353.5	25.7	270	2	S56160	mast cell tryptase

103	353	25.7	274	2	JC4171	trypsin (EC 3.4.21)	176	320.5	23.3	247	1	PRMSCL	granzyme B (EC 3.4
104	352	25.6	260	2	A45061	granzyme A (EC 3.4	177	319.5	23.3	559	1	A29941	t-plasminogen acti
105	352	25.6	461	1	JX0210	protein C (activat	178	319	23.2	1034	1	A53663	enteropeptidase (E
106	351	25.5	456	1	KXBO	protein C (activat	179	318.5	23.2	460	2	B61545	plasmin (EC 3.4.21
107	349.5	25.4	269	2	B26823	pancreatic elastas	180	318	23.1	265	2	T10495	chymotrypsin (EC 3
108	348	25.3	267	2	S40006	trypsin (EC 3.4.21	181	318	23.1	271	2	I46580	factor IX - pig (f
109	347	25.3	461	1	KXHU	protein C (activat	182	318	23.1	274	2	I47078	coagulation factor
110	346.5	25.2	244	2	S26042	chymase (EC 3.4.21	183	318	23.1	618	2	A35827	thrombin (EC 3.4.2
111	346.5	25.2	461	1	S18994	protein C (activat	184	317.5	23.1	245	1	KYBOB	chymotrypsin (EC 3
112	344	25.0	275	2	B35863	trypsin (EC 3.4.2	185	317.5	23.1	246	2	A32692	cytotoxic T-lympho
113	343.5	25.0	273	2	A47246	trypsin (EC 3.4.2	186	317	23.1	249	2	A55634	granzyme M (EC 3.4
114	343.5	25.0	274	2	S35339	trypsin (EC 3.4.21	187	316.5	23.0	246	1	A46504	chymase (EC 3.4.21
115	343	25.0	275	2	A32410	trypsin (EC 3.4.2	188	315.5	23.0	254	1	TRWV3Y	trypsin-like prote
116	342.5	24.9	558	2	JC5878	plasma hyaluronan-	189	315.5	23.0	266	1	ELRT1	pancreatic elastas
117	342.5	24.9	810	1	PLHU	plasmin (EC 3.4.21	190	315.5	23.0	392	1	A30100	serine proteinase
118	342	24.9	275	2	C35863	trypsin (EC 3.4.2	191	315.5	23.0	492	1	EXBO	coagulation factor
119	342	24.9	275	2	A35863	trypsin (EC 3.4.2	192	315	22.9	617	2	S43259	granzyme-like prot
120	341.5	24.9	258	2	I56220	trypsin (EC 3.4.2	193	315	22.9	617	2	S10511	thrombin (EC 3.4.2
121	340.5	24.8	246	2	B38678	mast cell proteinase	194	315	22.9	686	1	A59271	Ra-reactive factor
122	339.5	24.7	258	2	A45161	serine proteinase	195	314	22.9	275	2	S40005	trypsin (EC 3.4.21
123	339.5	24.7	267	4	A56615	probable pancreati	196	313	22.8	613	2	S15468	complement C3b/C4b
124	339	24.7	257	2	B45061	granzyme A (EC 3.4	197	313	22.8	855	2	JC7731	membrane-bound arg
125	339	24.7	461	1	KFHU1	coagulation factor	198	312.5	22.7	274	2	S40004	trypsin-related pr
126	339	24.7	625	1	KFHU1	coagulation factor	199	312.5	22.7	615	1	KFHU12	coagulation factor
127	338	24.6	625	1	TBBO	thrombin (EC 3.4.2	200	311.5	22.7	761	2	JC5759	brain-specific ser
128	337.5	24.6	238	1	TRWV5Y	trypsin-like prote	201	311	22.6	261	2	S40162	cathepsin G (EC 3.
129	337.5	24.6	264	2	S65663	granzyme 3 (EC 3.4	202	311	22.6	431	2	S47538	acrosin (EC 3.4.21
130	337	24.5	434	1	A35005	u-plasminogen acti	203	311	22.6	433	1	JN0560	u-plasminogen acti
131	337	24.5	812	1	PLMS	plasmin (EC 3.4.21	204	311	22.6	1035	1	A43090	enteropeptidase (E
132	336.5	24.5	251	2	T10262	mast cell serine p	205	310.5	22.6	247	1	PRRTG	mast cell proteina
133	336.5	24.5	251	2	PC1235	29K serine protein	206	310.5	22.6	559	1	A35029	t-plasminogen acti
134	336.5	24.5	638	1	KQMSPL	plasma kallikrein	207	310	22.6	275	2	I46712	factor IX - rabbit
135	336	24.5	416	1	KFBO	coagulation factor	208	309.5	22.5	482	1	EXRT	coagulation factor
136	336	24.5	790	1	PLPG	plasmin (EC 3.4.21	209	307	22.3	250	2	S55493	serine proteinase
137	335.5	24.4	258	4	S70439	pancreatic elastas	210	307	22.3	259	1	S49129	chymotrypsin (EC 3
138	333	24.2	245	1	KYBOA	chymotrypsin (EC 3	211	307	22.3	417	1	S00845	hepsin (EC 3.4.21.
139	333	24.2	285	2	I48144	coagulation factor	212	306.5	22.3	375	1	A23689	limulus clotting e
140	332.5	24.2	638	1	KQRTPL	plasma kallikrein	213	305.5	22.2	236	2	I42696	thrombin (EC 3.4.2
141	332.5	24.2	810	2	I46260	plasmin (EC 3.4.21	214	305	22.2	281	1	A61021	granzyme B (EC 3.4
142	332.5	24.2	810	2	B30848	plasmin (EC 3.4.21	215	304	22.1	149	1	KQMSM	tissue kallikrein
143	331.5	24.1	256	1	TRFF	trypsin-like prote	216	304	22.1	236	2	C42696	thrombin (EC 3.4.2
144	331.5	24.1	275	2	S40007	trypsin (EC 3.4.21	217	304	22.1	268	2	S68825	pancreatic elastas
145	331	24.1	263	1	KYRTB	chymotrypsin (EC 3	218	304	22.1	562	1	UKHUT	t-plasminogen acti
146	331	24.1	622	1	TBHU	thrombin (EC 3.4.2	219	303.5	22.1	244	2	A46721	chymase (EC 3.4.21
147	330.5	24.1	247	1	KYHUCM	chymase (EC 3.4.21	220	303.5	22.1	309	2	B49878	coagulation factor
148	330.5	24.1	560	1	JC4795	plasma hyaluronan-	221	303	22.1	196	2	T08808	hypothetical prote
149	330	24.0	282	2	I84621	coagulation factor	222	302.5	22.0	244	2	A34910	mast cell proteina
150	330	24.0	4548	1	S00657	apoprotein(a) (EC	223	302.5	22.0	273	2	S40003	trypsin-related pr
151	329.5	24.0	226	2	JE0151	myonase (EC 3.4.-.	224	302.5	22.0	1004	2	T30338	oviductin (EC 3.4.
152	329.5	24.0	237	2	S68702	trypsin (EC 3.4.2	225	302.5	22.0	1113	2	JE0315	low-density lipopr
153	329.5	24.0	269	2	C26823	pancreatic elastas	226	302	22.0	268	2	S68826	pancreatic elastas
154	329.5	24.0	1420	2	A32869	apolipoprotein(a)	227	302	22.0	394	2	JS0600	t-plasminogen acti
155	328.5	23.9	455	2	A61545	plasmin (EC 3.4.21	228	302	22.0	477	1	A34369	t-plasminogen acti
156	328.5	23.9	786	1	A47547	serine proteinase	229	302	22.0	477	2	JS0598	t-plasminogen acti
157	328	23.8	452	1	A30351	coagulation factor	230	301	21.9	255	2	A27122	cathepsin G (EC 3.
158	327.5	23.8	266	2	S54146	trypsin (EC 3.4.21	231	301	21.9	431	2	JS0599	t-plasminogen acti
159	327	23.8	244	2	S72219	chymotrypsin B - A	232	300.5	21.9	442	1	UKPG	u-plasminogen acti
160	327	23.8	259	2	S68424	allergen Der f III	233	300	21.8	245	2	A48598	kallikrein-like se
161	326.5	23.8	248	1	PRMSC2	granzyme C (EC 3.4	234	299.5	21.8	235	2	E42696	thrombin (EC 3.4.2
162	326.5	23.8	266	1	ELPG	pancreatic elastas	235	299.5	21.8	246	2	A38678	mast cell proteina
163	326	23.7	248	2	S33755	granzyme-like prot	236	299.5	21.8	258	1	S44184	chymotrypsin (EC 3
164	324	23.6	274	2	A45754	trypsin (EC 3.4.2	237	299.5	21.8	436	2	UX0172	acrosin (EC 3.4.21
165	324	23.6	459	2	JQ0419	coagulation factor	238	299	21.8	437	2	S18407	acrosin (EC 3.4.21
166	324	23.6	1019	1	A56318	enteropeptidase (E	239	298.5	21.7	191	2	S54115	complement factor
167	323.5	23.5	466	1	KFHU7	coagulation factor	240	298.5	21.7	249	1	A35842	chymase (EC 3.4.21
168	322	23.4	699	1	I54763	coagulation factor	241	298.5	21.7	270	2	B29934	pancreatic elastas
169	321.5	23.4	251	2	JC2125	Ra-reactive factor	242	298.5	21.7	407	1	KFBO7	coagulation factor
170	321	23.4	226	1	KCUF	chymase (EC 3.4.21	243	297	21.6	237	1	TRCY1	trypsin (EC 3.4.21
171	321	23.4	226	2	S69370	duodenase - bovine	244	297	21.6	260	2	S26043	chymase (EC 3.4.21
172	321	23.4	247	2	S64708	chymase (EC 3.4.21	245	297	21.6	418	2	A37344	acrosin (EC 3.4.21
173	321	23.4	248	2	A43520	natural killer cel	246	297	21.6	477	2	JS0597	t-plasminogen acti
174	321	23.4	269	2	B32410	mastocytoma protei	247	296.5	21.6	248	1	S01007	granzyme F (EC 3.4
175	321	23.4	655	1	A46688	hepatocyte growth	248	296	21.5	281	2	T13596	trypsin homolog -



249	295.5	21.5	239	2	G42696	thrombin (EC 3.4.2
250	295.5	21.5	433	1	UKMS	u-plasminogen acti
251	294	21.4	247	2	S23504	chymase (EC 3.4.21
252	294	21.4	303	2	T13598	trypsin homolog -
253	293.5	21.4	431	1	UKHU	u-plasminogen acti
254	293	21.3	234	2	F42696	thrombin (EC 3.4.2
255	293	21.3	247	2	S59135	mast cell proteina
256	293	21.3	265	2	A38894	serine proteinase
257	293	21.3	265	2	JS0260	serine proteinase
258	293	21.3	433	1	UKBAY	u-plasminogen acti
259	292.5	21.3	236	2	A28566	T-cell suppressor
260	291.5	21.2	216	1	KYVH20	chymotrypsin (EC 3
261	291	21.2	271	2	S41308	serine proteinase
262	289.5	21.1	248	2	A33412	cytotoxic T-lympho
263	289	21.0	583	2	A29154	complement factor
264	288.5	21.0	270	2	A29934	pancreatic elastas
265	288.5	21.0	1047	2	A55617	masquerade precurs
266	288	21.0	268	2	JQ1473	pancreatic elastas
267	288	21.0	421	2	S29599	acrosin (EC 3.4.21
268	287.5	20.9	235	2	H42696	thrombin (EC 3.4.2
269	287.5	20.9	603	2	S28941	coagulation factor
270	286.5	20.9	218	1	KYVH2C	chymotrypsin (EC 3
271	286	20.8	254	2	S35585	chymotrypsin-like
272	285.5	20.8	235	2	D42696	thrombin (EC 3.4.2
273	282.5	20.6	331	2	T27906	hypothetical prote
274	282	20.5	416	1	S33777	hepsin (EC 3.4.21.
275	280	20.4	254	2	S65465	trypsin-like prote
276	278.5	20.3	593	2	S45281	coagulation factor
277	277.5	20.2	266	2	JC4850	trypsin-like prote
278	276	20.1	430	1	A24702	serine proteinase
279	276	20.1	488	1	EXHU	coagulation factor
280	275.5	20.1	240	1	CPBOA3	procarboxypeptidas
281	275	20.0	237	2	S55378	serine proteinase
282	274.5	20.0	695	1	S05008	complement subcomp
283	273	19.9	247	2	S45113	granzyme-like prot
284	273	19.9	265	2	T15451	hypothetical prote
285	272.5	19.8	432	1	S18932	u-plasminogen acti
286	272	19.8	475	1	EXCH	coagulation factor
287	272	19.8	688	1	C1HUS	complement subcomp
288	271	19.7	2616	2	A57096	nudel protein prec
289	270	19.7	694	2	JC6554	complement subcomp
290	269.5	19.6	248	2	S33756	granzyme-like prot
291	269	19.6	256	1	PRHU3	proteinase 3 (EC 3
292	268.5	19.5	420	2	A55283	acrosin (EC 3.4.21
293	265	19.3	415	1	A34170	acrosin (EC 3.4.21
294	264.5	19.3	256	2	T10109	trypsin (EC 3.4.21
295	264.5	19.3	264	2	S32794	trypsin-like prote
296	263.5	19.2	251	1	TRHUAZ	azurocidin precurs
297	261.5	19.0	366	2	JE0105	testicular serine
298	261.5	19.0	421	1	S11674	acrosin (EC 3.4.21
299	259	18.9	248	2	S01006	cytotoxic T-lympho
300	258.5	18.8	252	2	A36172	procytotoxic T-lym
301	258.5	18.8	285	2	T35195	probable serine pr
302	257.5	18.7	254	2	S49329	trypsin-like prote
303	256	18.6	403	2	C82228	probable trypsin v
304	252	18.3	400	1	A48050	coagulation factor
305	248	18.0	367	2	JE0104	testicular serine
306	247	18.0	243	2	A56338	venom proteinase (
307	245	17.8	711	1	A47136	macrophage-stimula
308	244.5	17.8	716	1	A40332	macrophage-stimula
309	239.5	17.4	265	2	I48679	neutrophil elastas
310	237.5	17.3	232	2	S32398	serine proteinase
311	235.5	17.1	198	2	S06176	cytotoxic T-lympho
312	235.5	17.1	716	1	JC5061	macrophage-stimula
313	235	17.1	96	2	A05308	tissue kallikrein
314	235	17.1	230	2	A27802	hypodermin C (EC 3
315	234.5	17.1	219	1	TRPGAZ	azurocidin - pig
316	233	17.0	705	1	C1HURB	complement subcomp
317	231.5	16.8	230	2	I48685	mast cell proteina
318	227.5	16.6	272	2	JC4170	trypsin-like prote
319	227	16.5	259	1	TRSMG	trypsin (EC 3.4.21
320	226	16.4	728	1	JH0579	hepatocyte growth
321	225	16.4	548	2	D82175	probable trypsin v

322	220.5	16.0	267	1	ELHUL	leukocyte elastase
323	217.5	15.8	710	1	I51283	hepatocyte growth
324	216	15.7	728	1	A35644	hepatocyte growth
325	216	15.7	728	1	A60185	hepatocyte growth
326	204.5	14.9	177	2	S23505	chymase (EC 3.4.21
327	201	14.6	214	2	S17680	fibrinolytic prote
328	197.5	14.4	213	2	S17537	fibrinolytic prote
329	196	14.3	248	2	S49323	chymotrypsin (EC 3
330	192.5	14.0	763	2	I50807	complement factor
331	189.5	13.8	94	2	PC2013	tissue kallikrein
332	182	13.2	104	2	S15395	tissue kallikrein-
333	180	13.1	258	2	G02959	haptoglobin - rhes
334	179.5	13.1	149	2	S35208	serine proteinase
335	178	13.0	348	1	HPHUR	haptoglobin-relate
336	177	12.9	347	1	HPHU1	haptoglobin precur
337	177	12.9	406	1	HPHU2	haptoglobin precur
338	176.5	12.8	760	1	C2MS	classical-compleme
339	176	12.8	735	2	T35778	probable fusidic a
340	174.5	12.7	377	2	C88710	protein C43G2.5 [1
341	174	12.7	161	2	I48158	coagulation factor
342	174	12.7	330	2	B82415	probable serine pr
343	172	12.5	346	2	I36942	haptoglobin - chim
344	171	12.4	159	2	S35202	proteinase 2 - buf
345	171	12.4	258	2	I36945	haptoglobin Hp - c
346	171	12.4	345	2	I36941	haptoglobin - chim
347	170	12.4	347	2	G00006	haptoglobin - blac
348	169	12.3	329	1	HPDG	haptoglobin precur
349	168	12.2	66	2	I52972	kallikrein - mouse
350	168	12.2	154	2	S35207	proteinase 7 - buf
351	166	12.1	258	2	I36947	haptoglobin Hpp -
352	166	12.1	349	2	I36944	haptoglobin - chim
353	166	12.1	752	1	C2HU	complement C2 prec
354	165	12.0	161	2	I62744	coagulation factor
355	165	12.0	347	1	HPMS	haptoglobin precur
356	159.5	11.6	152	2	S35209	serine proteinase
357	159	11.6	126	2	A23473	chymotrypsin-like
358	158.5	11.5	264	2	A28942	pancreatic elastas
359	157.5	11.5	764	1	BBHU	complement factor
360	154.5	11.2	747	2	I51579	complement factor
361	153.5	11.2	761	1	BBMS	complement factor
362	152.5	11.1	159	2	I84615	coagulation factor
363	152	11.1	181	2	T08805	hypothetical prote
364	151.5	11.0	152	2	S35203	serine proteinase
365	148	10.8	81	2	A18966	tissue kallikrein
366	145.5	10.6	82	2	T46510	hypothetical prote
367	138.5	10.1	158	2	S35201	serine proteinase
368	138	10.0	153	2	S35204	proteinase 4 - buf
369	137	10.0	743	2	T34853	probable fusidic a
370	136.5	9.9	152	2	S35206	serine proteinase
371	135.5	9.9	46	2	I49416	glandular kallikre
372	132	9.6	347	1	HPRT	haptoglobin precur
373	129.5	9.4	396	1	KXBOZ	plasma protein 2 -
374	127.5	9.3	69	2	S28195	tissue kallikrein
375	127.5	9.3	72	2	S28196	tissue kallikrein
376	126	9.2	80	2	A05324	gamma- $\alpha$ -renin (EC 3.
377	123.5	9.0	137	2	S55364	serine proteinase
378	123.5	9.0	151	2	S35205	proteinase 5 - buf
379	122.5	8.9	75	2	A37002	catrobin I (EC 3
380	115.5	8.4	422	1	KXHUZ	plasma protein 2 p
381	114.5	8.3	85	2	S44461	elastase (EC 3.4.2
382	109.5	8.0	61	2	PS0049	serine proteinase
383	108	7.9	333	2	T15257	hypothetical prote
384	104.5	7.6	256	2	A56593	trypsin-related pr
385	104	7.6	49	2	B24696	tissue kallikrein
386	103.5	7.5	64	2	A30981	prostatic arginine
387	99.5	7.2	340	2	T34423	hypothetical prote
388	97	7.1	388	2	S34672	alkaline serine pr
389	96.5	7.0	416	2	AH2387	hypothetical prote
390	94.5	6.9	416	2	G71965	glycine hydroxymet
391	93.5	6.8	73	2	S44462	elastase (EC 3.4.2
392	93.5	6.8	299	1	PRSMBG	streptogrisin B (E
393	92.5	6.7	416	2	G64542	glycine hydroxymet
394	91	6.6	31	2	A18671	tissue kallikrein

395	90.5	6.6	48	2	A61331	trypsin (EC 3.4.21	468	78	5.7	4006	2	T09070	probable tenascin
396	90	6.6	1746	1	S19694	tenascin precursor	469	77.5	5.6	438	2	S53787	collagen alpha cha
397	90	6.6	2825	2	T14271	Doc4 protein, stre	470	77.5	5.6	921	2	S42617	collagen alpha 1(I
398	89	6.5	457	2	A53669	streptogrisin C (E	471	77.5	5.6	1669	1	CGMS4B	collagen alpha 1(I
399	89	6.5	1737	2	T00209	MEGF8 protein - hu	472	77.5	5.6	1691	1	CGHU6B	collagen alpha 6(I
400	88.5	6.4	2205	1	MNWVRN	nonstructural poly	473	77.5	5.6	2907	2	A57278	fibrillin-2 precur
401	88.5	6.4	3002	2	A47221	fibrillin 1 precur	474	77	5.6	517	2	T47134	hypothetical prote
402	87.5	6.4	278	2	AH0282	probable pepetidas	475	77	5.6	553	2	F75407	probable transport
403	87.5	6.4	1582	2	T15308	hypothetical prote	476	77	5.6	668	2	A41234	melanocyte-specifi
404	86.5	6.3	34	2	I49417	nerve growth facto	477	77	5.6	710	2	T31502	hypothetical prote
405	86.5	6.3	38	2	I70029	kallikrein, exon 2	478	77	5.6	1104	2	I38869	transcription fact
406	86.5	6.3	38	2	I70016	kallikrein - mouse	479	77	5.6	3566	1	A40701	tenascin-X precurs
407	86.5	6.3	38	2	I70036	kallikrein - mouse	480	76.5	5.6	295	2	A44984	collagen - nematod
408	86	6.3	70	2	A56784	kallikrein-like se	481	76.5	5.6	315	2	H83096	probable pyrophosp
409	86	6.3	502	2	A48679	differentiated ker	482	76.5	5.6	348	2	A34705	collagen - Caenorh
410	86	6.3	2704	2	S09118	G surface protein	483	76.5	5.6	382	2	PC2053	alkaline proteinas
411	85	6.2	398	2	B75254	acetate kinase - D	484	76.5	5.6	469	1	S29126	properdin precurs
412	85	6.2	411	2	T34585	probable secreted	485	76.5	5.6	1042	1	CGCH1S	collagen alpha 1(I
413	85	6.2	2718	2	A23475	G surface protein	486	76.5	5.6	1453	2	S21626	collagen alpha 1(I
414	84.5	6.1	287	2	T22637	hypothetical prote	487	76.5	5.6	1532	2	A61262	collagen alpha 1(X
415	84.5	6.1	1023	2	T30257	IgG Fc binding pro	488	76	5.5	257	2	T52298	squamosa promoter
416	84.5	6.1	2871	2	A55567	fibrillin I - bovi	489	76	5.5	301	2	C84474	hypothetical prote
417	84	6.1	273	2	E85765	hypothetical prote	490	76	5.5	361	2	S30325	hypothetical prote
418	84	6.1	305	2	S44767	C29E4.1 protein -	491	76	5.5	465	2	AF2949	ornithine decarbox
419	84	6.1	458	2	T36442	probable serine pr	492	76	5.5	512	2	E98333	probable ornithine
420	84	6.1	725	2	E96596	hypothetical prote	493	76	5.5	608	2	T05442	glycine-rich prote
421	83.5	6.1	133	2	T17300	hypothetical prote	494	76	5.5	677	2	S23296	collagen alpha 2(I
422	83.5	6.1	788	2	A37057	integrin beta-6 ch	495	76	5.5	920	2	B34493	collagen alpha 1(I
423	83.5	6.1	1433	2	A46053	bullous pemphigoid	496	76	5.5	986	1	OYURGA	collagen alpha 1(I
424	83	6.0	266	2	T21597	hypothetical prote	497	76	5.5	3396	1	A42551	speract receptor p
425	83	6.0	273	2	H64915	Putative protease	498	75.5	5.5	396	2	S22909	genome polyprotein
426	82.5	6.0	522	2	T29767	hypothetical prote	499	75.5	5.5	481	2	A35628	interleukin-3 rece
427	82.5	6.0	644	2	C75457	alpha-amylase - De	500	75.5	5.5	596	2	T26950	loricrin - mouse
428	82.5	6.0	4936	2	AH2515	hypothetical prote	501	75.5	5.5	621	2	T50024	hypothetical prote
429	82	6.0	90	2	JE0210	proteainase (EC 3.4	502	75.5	5.5	653	2	A46362	hypothetical prote
430	82	6.0	357	2	T21152	hypothetical prote	503	75.5	5.5	677	2	T37310	collagen alpha 2(I
431	82	6.0	418	2	A46076	staphylytic prot	504	75.5	5.5	688	2	A53330	collagen alpha 1(I
432	82	6.0	418	2	F83411	LasA proteinase pr	505	75.5	5.5	697	2	T18681	hypothetical prote
433	81.5	5.9	244	2	JC4708	gelatin-binding 28	506	75.5	5.5	1142	2	JX0369	collagen alpha 1(X
434	81.5	5.9	323	2	T27450	hypothetical prote	507	75	5.5	291	2	T20083	hypothetical prote
435	81.5	5.9	779	1	CGBO1S	collagen alpha 1(I	508	75	5.5	291	2	T26576	hypothetical prote
436	81.5	5.9	2229	2	T16199	hypothetical prote	509	75	5.5	310	2	I50696	collagen alpha 1(I
437	81	5.9	247	2	T26688	hypothetical prote	510	75	5.5	437	2	S05478	properdin - mouse
438	81	5.9	428	2	T24769	hypothetical prote	511	75	5.5	809	1	IJBODD	desmocollin 2b pre
439	80.5	5.9	283	2	T29837	hypothetical prote	512	75	5.5	863	1	IJBODC	desmocollin 2a pre
440	80.5	5.9	290	2	T46470	hypothetical prote	513	75	5.5	864	1	EART	elastin precursor
441	80.5	5.9	294	2	T29839	hypothetical prote	514	75	5.5	902	2	T26775	hypothetical prote
442	80.5	5.9	812	2	S31521	collagen COLF1 - f	515	75	5.5	1140	2	AE0180	probable membrane
443	80.5	5.9	1464	1	CGHU1S	collagen alpha 1(I	516	75	5.5	1236	1	VHWVWE	structural polypro
444	80.5	5.9	2871	2	A55624	fibrillin-1 precur	517	75	5.5	1514	2	T52080	multi resistance p
445	80	5.8	248	2	A48853	pulmonary surfacta	518	75	5.5	1752	2	A45407	collagen alpha 3(I
446	80	5.8	333	2	T23618	hypothetical prote	519	74.5	5.4	177	2	AB3269	outer membrane lip
447	79.5	5.8	550	2	E90723	probable fumarate	520	74.5	5.4	246	2	S30144	osmotin-like prote
448	79.5	5.8	550	2	E85574	probable fumarate	521	74.5	5.4	601	2	G70983	probable glycosyl
449	79	5.7	274	2	T20435	hypothetical prote	522	74.5	5.4	638	1	A31845	nitrous-oxide redu
450	79	5.7	295	2	T19220	hypothetical prote	523	74.5	5.4	791	2	G71885	probable iron-regu
451	79	5.7	333	2	T20436	hypothetical prote	524	74.5	5.4	832	2	A31246	neurogenic protein
452	79	5.7	782	2	A61625	tenascin-like prot	525	74.5	5.4	833	2	S19087	gene Delta protein
453	79	5.7	921	2	S40495	collagen alpha 1(I	526	74.5	5.4	880	2	S00670	neurogenic repetit
454	79	5.7	1758	2	T29350	hypothetical prote	527	74.5	5.4	931	2	S13580	collagen alpha 1(I
455	79	5.7	1759	2	T29351	collagen alpha 2(I	528	74.5	5.4	1496	1	CGHU2V	collagen alpha 2(V
456	78.5	5.7	294	2	T22639	hypothetical prote	529	74.5	5.4	1690	1	CGHU1B	collagen alpha 4(I
457	78.5	5.7	310	2	T22641	hypothetical prote	530	74.5	5.4	1763	2	S16366	collagen alpha 2(I
458	78.5	5.7	504	2	T34995	probable integral	531	74	5.4	246	2	S29328	complement subcomp
459	78.5	5.7	1315	2	A56101	collagen alpha 1(X	532	74	5.4	248	1	LNRTPS	pulmonary surfacta
460	78.5	5.7	1774	2	B56101	collagen alpha 1(X	533	74	5.4	273	2	AE0682	probable secreted
461	78.5	5.7	2115	2	S38480	nonstructural prot	534	74	5.4	302	2	A31921	collagen dpy-13 pr
462	78.5	5.7	2214	2	T16305	hypothetical prote	535	74	5.4	325	2	T18594	hypothetical prote
463	78.5	5.7	4135	2	T42629	tenascin-X - bovin	536	74	5.4	457	2	T04226	hypothetical prote
464	78.5	5.7	4545	1	S25111	alpha-2-macroglubu	537	74	5.4	470	2	D41977	retinoid receptor
465	78	5.7	300	2	T36768	secreted serine pr	538	74	5.4	513	2	S11439	cellulose 1,4-beta
466	78	5.7	359	2	E83312	hypothetical prote	539	74	5.4	566	2	S69887	hemagglutinin prec
467	78	5.7	394	2	T33641	hypothetical prote	540	74	5.4	614	2	T33149	hypothetical prote

541	74	5.4	886	2	I50694	collagen alpha 1(I	614	71.5	5.2	895	2	T49010	hypothetical prote
542	74	5.4	1124	1	I58388	protein-tyrosine k	615	71.5	5.2	918	2	JC4361	scavenger receptor
543	74	5.4	1413	2	T26467	hypothetical prote	616	71	5.2	181	2	S56532	hypothetical 20K p
544	74	5.4	1670	1	CGHU3B	collagen alpha 3(I	617	71	5.2	316	2	S25264	virK protein - Shi
545	74	5.4	1677	2	T14267	Xin protein, stage	618	71	5.2	359	2	E70606	probable regulator
546	73.5	5.3	246	2	T16403	hypothetical prote	619	71	5.2	407	2	AI0595	imidazolonepropion
547	73.5	5.3	294	2	T29838	hypothetical prote	620	71	5.2	458	2	T31631	hypothetical prote
548	73.5	5.3	305	2	B84413	hypothetical prote	621	71	5.2	490	2	T37884	transcription fact
549	73.5	5.3	321	2	T28760	hypothetical prote	622	71	5.2	497	2	B42827	interleukin enhanc
550	73.5	5.3	346	2	JA0159	cysteine proteinas	623	71	5.2	575	2	A97635	adenine deaminase
551	73.5	5.3	411	2	A65184	arylsulfatase acti	624	71	5.2	575	2	AC2858	adenine deaminase
552	73.5	5.3	482	2	AE0839	succinate-semialde	625	71	5.2	639	2	D70931	hypothetical glyci
553	73.5	5.3	483	2	D83613	cellulose-1,4-beta	626	71	5.2	818	2	B75606	hypothetical prote
554	73.5	5.3	525	1	S38794	collagen alpha 1(X	627	71	5.2	883	2	T51221	hypothetical prote
555	73.5	5.3	680	1	CGHU1D	antigen Em100 - E1	628	71	5.2	1230	2	E64664	outer membrane pro
556	73.5	5.3	724	2	A48569	iron-regulated out	629	71	5.2	1391	2	T20406	hypothetical prote
557	73.5	5.3	791	2	D64629	collagen alpha 1(X	630	71	5.2	1691	1	S22917	collagen alpha 5(I
558	73.5	5.3	1806	1	CGHU1E	cerastocytin (EC 3	631	71	5.2	1717	1	A45558	epidermal growth f
559	73	5.3	50	2	S55674	hypothetical prote	632	71	5.2	2164	1	GNNY89	genome polyprotein
560	73	5.3	295	2	T22833	probable secreted	633	71	5.2	2531	2	S18188	notch protein homo
561	73	5.3	360	2	T36763	probable transmemb	634	71	5.2	2531	2	T16743	hypothetical prote
562	73	5.3	508	2	B70865	metalloproteinase	635	71	5.2	3512	2	T17121	CPY protein - midg
563	73	5.3	597	2	S71352	melanoma-associate	636	70.5	5.1	238	2	S28001	osmotin-like prote
564	73	5.3	662	2	I38400	tryptophan synthas	637	70.5	5.1	284	2	T29528	hypothetical prote
565	73	5.3	707	1	TSBYAB	transcription acti	638	70.5	5.1	290	2	AE1176	fructokinases homo
566	73	5.3	728	2	S43768	hypothetical prote	639	70.5	5.1	325	2	T06784	GTP-binding protei
567	73	5.3	767	2	T05662	nitrate reductase	640	70.5	5.1	325	2	T09613	hypothetical prote
568	73	5.3	881	2	S25445	230k bullous pemph	641	70.5	5.1	339	2	T22607	cysteine proteinas
569	73	5.3	997	2	A60776	epidermal growth f	642	70.5	5.1	356	2	S66348	collagen short cha
570	73	5.3	1339	2	JC4387	collagen alpha 1(I	643	70.5	5.1	366	2	S11449	alpha-lytic protei
571	73	5.3	1744	2	S40991	genome polyprotein	644	70.5	5.1	396	1	TRYXB4	probable secreted
572	73	5.3	2207	1	GNNY5P	notch protein homo	645	70.5	5.1	400	2	T35106	collagen 13, nonfi
573	73	5.3	2555	2	A40043	genome polyprotein	646	70.5	5.1	423	2	A41207	probable transcrip
574	73	5.3	3061	1	JN0545	intrinsic factor-B	647	70.5	5.1	585	2	T37526	polyketide hydroxy
575	73	5.3	3623	2	T08618	trypsin/factor XII	648	70.5	5.1	627	2	T35608	hypothetical prote
576	72.5	5.3	155	1	T1ZM1	probable chaperone	649	70.5	5.1	630	2	T43460	elastin precursor
577	72.5	5.3	230	2	D85553	probable chaperone	650	70.5	5.1	860	1	EAMS	collagen alpha 1(V
578	72.5	5.3	230	2	A90703	molecular chaperon	651	70.5	5.1	920	2	A45748	kinase-related tra
579	72.5	5.3	230	2	B64785	dihydrodipicolinat	652	70.5	5.1	1342	2	A36223	collagen alpha 2(I
580	72.5	5.3	286	2	C81681	hypothetical prote	653	70.5	5.1	1414	1	S23809	collagen alpha 1(I
581	72.5	5.3	302	2	T32872	2-nitrotoluene red	654	70.5	5.1	1486	1	B40333	collagen alpha-4 c
582	72.5	5.3	328	2	JC5350	probable secreted	655	70.5	5.1	1747	2	A54121	collagen alpha 2 f
583	72.5	5.3	362	2	T35287	Regulator of chrom	656	70.5	5.1	3198	2	A43426	chlorophyll a/b-bi
584	72.5	5.3	488	2	T47697	PF20 protein, micr	657	70	5.1	261	2	S40210	collagen col-19 -
585	72.5	5.3	606	2	T08180	telomerase catalyt	658	70	5.1	283	2	JS0170	collagen alpha cha
586	72.5	5.3	1132	2	T03844	procollagen type V	659	70	5.1	285	2	S60598	hypothetical prote
587	72.5	5.3	1497	2	I49607	glutamate synthase	660	70	5.1	300	2	T19929	hypothetical prote
588	72.5	5.3	1514	2	T34869	hypothetical prote	661	70	5.1	304	2	T26185	hypothetical prote
589	72	5.2	207	2	T46415	probable O-methylt	662	70	5.1	304	2	T26184	hypothetical prote
590	72	5.2	220	2	T18553	hypothetical prote	663	70	5.1	313	2	T26465	probable transcrip
591	72	5.2	229	2	D95398	Ubq protein - frui	664	70	5.1	315	2	C95941	hemagglutinin - in
592	72	5.2	258	2	A29259	streptogrisin D (E	665	70	5.1	343	2	JQ2370	potential oncogene
593	72	5.2	392	2	A56123	integrin beta-6 ch	666	70	5.1	389	2	I49263	Wnt10b protein pre
594	72	5.2	577	2	B37057	protein F25E5.7 [i	667	70	5.1	395	1	T45547	arylsulfatase acti
595	72	5.2	673	2	F89101	probable bacteriop	668	70	5.1	402	2	H82228	imidazolonepropion
596	72	5.2	691	2	T44543	receptor kinase-li	669	70	5.1	485	2	F97228	glu-trNAGln amidot
597	72	5.2	814	2	T49207	hypothetical prote	670	70	5.1	548	2	H82432	sucrose-6-phosphat
598	72	5.2	957	2	T15976	jagged protein pre	671	70	5.1	560	2	D84205	hypothetical prote
599	72	5.2	1220	2	A56136	genome polyprotein	672	70	5.1	561	2	C75543	6-aminohexanoate-c
600	72	5.2	2150	1	GNNYH2	genome polyprotein	673	70	5.1	561	2	TGRT1S	collagen alpha 1(I
601	72	5.2	2194	1	GNNYE7	genome polyprotein	674	70	5.1	671	1	CGRT1S	collagen alpha 1(X
602	72	5.2	2205	1	GNNY2W	collagen homolog A	675	70	5.1	674	2	S23297	hypothetical prote
603	71.5	5.2	58	2	A45526	hypothetical prote	676	70	5.1	798	2	T28906	sag polyprotein -
604	71.5	5.2	236	2	T24799	chymotrypsin-like	677	70	5.1	863	2	A53034	envelope protein p
605	71.5	5.2	283	2	JC5579	hypothetical prote	678	70	5.1	877	2	S49197	hypothetical prote
606	71.5	5.2	284	2	G70732	probable thiosulfa	679	70	5.1	938	2	C84480	protein F14N23.5 [
607	71.5	5.2	297	2	T18638	hypothetical prote	680	70	5.1	1188	2	D86236	probable large Pro
608	71.5	5.2	305	2	T20906	hypothetical prote	681	70	5.1	1366	2	T35985	scavenger receptor
609	71.5	5.2	466	2	I39707	probable indoleace	682	70	5.1	2043	2	T18524	genome polyprotein
610	71.5	5.2	524	2	T04623	cruciferin F20O9.2	683	70	5.1	2206	1	GNNY4P	genome polyprotein
611	71.5	5.2	547	2	T29717	env polyprotein pr	684	70	5.1	2206	2	GNNY27	genome polyprotein
612	71.5	5.2	665	1	VCMVKA	hypothetical prote	685	70	5.1	2206	2	S03822	perlecan precursor
613	71.5	5.2	793	2	AH2126		686	70	5.1	4391	2	A38096	



687 69.5 5.1 126 2 S47010 Ig heavy chain V4.  
688 69.5 5.1 184 2 E82345 probable galactosy  
689 69.5 5.1 244 1 LNMSMC mannose-binding le  
690 69.5 5.1 248 1 LNDGSP pulmonary surfacta  
691 69.5 5.1 250 2 S30157 osmotin precursor  
692 69.5 5.1 275 2 A84179 endonuclease IV [i  
693 69.5 5.1 303 2 T19289 hypothetical prote  
694 69.5 5.1 337 2 T23794 hypothetical prote  
695 69.5 5.1 353 2 S16785 hemagglutinin - in  
696 69.5 5.1 356 2 S16907 collagen alpha 1(I  
697 69.5 5.1 382 2 S20375 collagen alpha 3(V  
698 69.5 5.1 432 2 F96919 ABC transporter (p  
699 69.5 5.1 466 2 T06416 cysteine proteinas  
700 69.5 5.1 482 2 S76475 hypothetical prote  
701 69.5 5.1 545 2 C82617 NH3-dependent NAD  
702 69.5 5.1 656 2 JC2005 integrin beta-5 ch  
703 69.5 5.1 739 2 C87559 phosphoribosylform  
704 69.5 5.1 749 2 I38488 trophinin - human  
705 69.5 5.1 1024 2 S18251 collagen alpha 1(X  
706 69.5 5.1 1181 2 C97851 DNA-directed DNA p  
707 69.5 5.1 1418 2 T45467 collagen alpha 1(I  
708 69.5 5.1 1464 2 S59856 collagen alpha 1(I  
709 69.5 5.1 1487 1 CGHU6C collagen alpha 1(I  
710 69.5 5.1 1603 2 S23810 collagen alpha 1(X  
711 69.5 5.1 1986 2 S28353 probable polyketid  
712 69.5 5.1 2019 1 JQ1322 tenascin precursor  
713 69.5 5.1 2201 2 A32160 tenascin-C - human  
714 69 5.0 38 2 T01677 pseudo-kallikrein  
715 69 5.0 224 2 S06545 finger protein (cl  
716 69 5.0 239 1 LNMSMA mannose-binding le  
717 69 5.0 290 2 T24586 hypothetical prote  
718 69 5.0 290 2 T24590 hypothetical prote  
719 69 5.0 294 2 T21668 hypothetical prote  
720 69 5.0 297 1 PRSMAG streptogrisin A (E  
721 69 5.0 327 2 S48839 guanine nucleotide  
722 69 5.0 329 2 B83162 molybdopterin bios  
723 69 5.0 334 1 S74957 cytochrome c-type  
724 69 5.0 395 2 S41035 hypothetical prote  
725 69 5.0 399 2 H84717 hypothetical prote  
726 69 5.0 406 2 A47696 acetamidase - Myco  
727 69 5.0 435 2 T39719 beta transducin -  
728 69 5.0 438 2 T50991 hypothetical prote  
729 69 5.0 441 2 A45565 cysteine proteinas  
730 69 5.0 469 2 A24450 collagen alpha 2(V  
731 69 5.0 523 2 B95922 hypothetical nucle  
732 69 5.0 532 2 F70580 hypothetical glyci  
733 69 5.0 567 1 C55516 hydrogenase (EC 1.  
734 69 5.0 567 2 G85958 probable large sub  
735 69 5.0 567 2 G91113 NADH2 dehydrogenas  
736 69 5.0 613 2 T11464 collagen alpha 2(V  
737 69 5.0 635 2 A57131 probable Tail-like  
738 69 5.0 682 2 D84579 URBS1 protein - sm  
739 69 5.0 950 2 S27473 collagen alpha 2(I  
740 69 5.0 1366 1 CGHU2S collagen alpha 1(I  
741 69 5.0 1669 1 CGHU4B hypothetical prote  
742 69 5.0 1749 2 S75071 laminin beta-1 cha  
743 69 5.0 1786 1 MMHUB1 genome polypotein  
744 69 5.0 2207 2 S09553 protein-tyrosine-p  
745 69 5.0 2209 1 GNNY2P ALR protein - huma  
746 69 5.0 2450 2 S71625 ALR protein - huma  
747 69 5.0 4957 2 T03455 ferredoxin XF1964  
748 69 5.0 5262 2 T03454 vasotocin 2 / neur  
749 68.5 5.0 127 2 F82617 pathogenesis-relat  
750 68.5 5.0 155 2 B32669 osmotin-like prote  
751 68.5 5.0 233 2 S31829 collagen alpha 1(V  
752 68.5 5.0 250 2 S25114 hypothetical prote  
753 68.5 5.0 252 2 A55047 fructokinases homo  
754 68.5 5.0 285 2 T18814 hypothetical prote  
755 68.5 5.0 290 2 A11533 fructokinases  
756 68.5 5.0 323 2 T19142 hypothetical prote  
757 68.5 5.0 329 2 T32783 hypothetical prote  
758 68.5 5.0 336 1 S76928 probable aryl alco  
759 68.5 5.0 337 2 A72042 conserved hypothet

760 68.5 5.0 337 2 H86582 CT 368 hypothetical  
761 68.5 5.0 357 2 H89819 conserved hypothet  
762 68.5 5.0 372 2 S60207 fomF protein - Str  
763 68.5 5.0 412 2 G86003 probable transport  
764 68.5 5.0 412 2 A91158 probable transport  
765 68.5 5.0 412 2 B65134 protein transport  
766 68.5 5.0 427 2 S57776 cysteine proteinas  
767 68.5 5.0 487 2 AF2692 MFS permease [impo  
768 68.5 5.0 528 2 B97474 hypothetical prote  
769 68.5 5.0 537 2 B33485 spore coat protein  
770 68.5 5.0 544 2 G87330 conserved hypothet  
771 68.5 5.0 547 2 A36046 collagen alpha cha  
772 68.5 5.0 575 2 JC7727 4-alpha-D-{(1->4)-  
773 68.5 5.0 579 2 B45266 MPL-K protein prec  
774 68.5 5.0 634 1 S24384 nitrous-oxide redu  
775 68.5 5.0 635 2 A45266 MPL-P protein prec  
776 68.5 5.0 673 1 CGBO6C collagen alpha 1(I  
777 68.5 5.0 674 2 S13301 collagen alpha 1(X  
778 68.5 5.0 677 2 F95910 probable membrane-  
779 68.5 5.0 744 1 A34246 collagen alpha 1(V  
780 68.5 5.0 744 1 S23298 collagen alpha 1(V  
781 68.5 5.0 744 2 S15435 collagen alpha 1(V  
782 68.5 5.0 888 2 S28791 collagen alpha 1(X  
783 68.5 5.0 915 2 T21773 hypothetical prote  
784 68.5 5.0 927 2 T21772 hypothetical prote  
785 68.5 5.0 937 2 I53282 gene PACE4 protein  
786 68.5 5.0 1049 1 CGBO7S collagen alpha 1(I  
787 68.5 5.0 1419 2 A41182 collagen alpha 1(I  
788 68.5 5.0 1487 2 B41182 collagen alpha 1(I  
789 68.5 5.0 2206 1 GNNY21 genome polypotein  
790 68.5 5.0 2403 2 A59386 sanko - human  
791 68.5 5.0 2482 2 I48922 cation-independent  
792 68.5 5.0 2483 1 A49617 insulin-like growt  
793 68.5 5.0 2560 1 I40457 peptide synthetase  
794 68.5 5.0 2715 2 T13049 eyelid - fruit fly  
795 68.5 5.0 3106 1 S53868 laminin alpha-2 ch  
796 68.5 5.0 4544 1 S02392 alpha-2-macroglobu  
797 68.5 5.0 4660 2 T42737 gp330 protein prec  
798 68 4.9 175 1 A60010 early E1A 20K prot  
799 68 4.9 177 2 S37749 collagen alpha 2(X  
800 68 4.9 229 1 S54799 nitrile hydratase  
801 68 4.9 237 2 A88640 protein C34H4.4 [i  
802 68 4.9 248 1 LNHUMC mannose-binding le  
803 68 4.9 272 2 H87075 probable conserved  
804 68 4.9 289 2 T27708 hypothetical prote  
805 68 4.9 297 2 T46864 nicotinate-nucleot  
806 68 4.9 330 2 T26004 hypothetical prote  
807 68 4.9 343 1 HMIV7A hemagglutinin HA1  
808 68 4.9 349 2 D72175 G2R protein - vari  
809 68 4.9 354 2 A35788 hemagglutinin - in  
810 68 4.9 358 2 T26281 hypothetical prote  
811 68 4.9 384 2 S46110 hypothetical prote  
812 68 4.9 387 2 B49175 Motch A protein -  
813 68 4.9 404 2 A54871 Gal beta-1, 3GalNA  
814 68 4.9 412 2 JC6317 glutamate dehydrog  
815 68 4.9 447 2 F82862 conjugal transfer  
816 68 4.9 453 2 S49168 beta tubulin 1 - r  
817 68 4.9 460 2 A39938 phosphotransferase  
818 68 4.9 484 2 F98208 succinate-semialde  
819 68 4.9 484 2 AC3078 aldehyde dehydroge  
820 68 4.9 490 2 E95316 succinate-semialde  
821 68 4.9 543 2 A41285 interleukin enhanc  
822 68 4.9 566 1 HMIV hemagglutinin prec  
823 68 4.9 566 1 HMIV17 hemagglutinin prec  
824 68 4.9 605 2 T15291 sphingomyelin phos  
825 68 4.9 631 2 JC2345 kexin-like protein  
826 68 4.9 656 2 G85731 Rhs element associ  
827 68 4.9 680 2 S31216 collagen alpha 1(X  
828 68 4.9 724 2 T27858 probable peroxidas  
829 68 4.9 726 2 T35865 probable cyclase -  
830 68 4.9 743 1 S23779 collagen alpha 1(V  
831 68 4.9 754 2 A55267 collagen alpha 5(I  
832 68 4.9 756 2 S67433 hypothetical prote

833	68	4.9	759	2	B70585	hypothetical prote	906	67	4.9	651	2	A26581	beta-glucuronidase
834	68	4.9	864	2	A48266	protein-tyrosine k	907	67	4.9	653	2	G96675	hypothetical prote
835	68	4.9	972	2	A30363	glycoprotein GP330	908	67	4.9	686	2	JC7569	Delta-4 protein -
836	68	4.9	1223	2	T17345	hypothetical prote	909	67	4.9	737	2	S65758	nitrate reductase
837	68	4.9	1331	2	S05011	calcium channel al	910	67	4.9	756	2	AH1022	arginine decarboxy
838	68	4.9	1400	2	E90886	RhsE core protein	911	67	4.9	884	2	T18649	hypothetical prote
839	68	4.9	1493	2	A44224	DNA repair helicase	912	67	4.9	919	2	T16150	hypothetical prote
840	68	4.9	1786	1	MMSB1	laminin beta-1 cha	913	67	4.9	1012	2	T13603	probable N-methyl-
841	68	4.9	2100	2	T03223	probable polyketid	914	67	4.9	1027	2	S28774	collagen alpha cha
842	68	4.9	2209	1	GNNY3P	genome polypeptin	915	67	4.9	1034	2	JC5598	mucin - rat
843	68	4.9	2767	1	UIHU	thyroglobulin prec	916	67	4.9	1051	2	A35763	collagen alpha 2 c
844	67.5	4.9	73	1	HPRB	haptoglobin precur	917	67	4.9	1064	2	A40136	fibropellin Ia - s
845	67.5	4.9	242	2	AG1868	hypothetical prote	918	67	4.9	1196	1	DNBEHF	DNA-binding protei
846	67.5	4.9	247	1	LNRBPS	pulmonary surfacta	919	67	4.9	1196	1	DNBEV1	major DNA-binding
847	67.5	4.9	286	2	S34665	collagen, cuticula	920	67	4.9	1373	1	A43291	collagen alpha 2(I
848	67.5	4.9	296	2	T21070	hypothetical prote	921	67	4.9	1466	1	CGHU7L	collagen alpha 1(I
849	67.5	4.9	307	2	T16842	hypothetical prote	922	67	4.9	1632	2	C70752	probable ctpI prot
850	67.5	4.9	315	2	T34932	hypothetical prote	923	67	4.9	1705	2	S51672	adenylate cyclase
851	67.5	4.9	315	2	AE2384	hypothetical prote	924	67	4.9	1747	2	A45974	collagen alpha 1(X
852	67.5	4.9	325	2	S02170	collagen alpha 1(I	925	67	4.9	1761	2	T13990	collagen type IV a
853	67.5	4.9	330	2	S46657	collagen alpha 1(X	926	67	4.9	1775	2	A31893	collagen alpha 1(I
854	67.5	4.9	337	2	A83026	hypothetical prote	927	67	4.9	1857	2	S31212	collagen alpha 1(X
855	67.5	4.9	339	2	E82211	conserved hypothet	928	67	4.9	1888	2	S78476	collagen alpha 1(X
856	67.5	4.9	356	2	A25918	thrombomodulin - b	929	67	4.9	2269	1	JQ1750	genome polyprotein
857	67.5	4.9	369	2	T02150	probable (S)-2-hyd	930	67	4.9	2524	2	A35844	Xotch protein - Af
858	67.5	4.9	383	2	T31771	hypothetical prote	931	67	4.9	3282	2	E82750	hemagglutinin-like
859	67.5	4.9	399	2	C95943	probable choline u	932	66.5	4.8	35	2	I49403	complement factor
860	67.5	4.9	412	2	AB1000	type II secretion	933	66.5	4.8	119	2	S41111	pancreatic ribonuc
861	67.5	4.9	451	2	S65162	hypothetical prote	934	66.5	4.8	122	2	JL0047	Ig heavy chain V r
862	67.5	4.9	528	2	T10622	hypothetical prote	935	66.5	4.8	140	2	A49045	Ig heavy chain V r
863	67.5	4.9	627	2	A70888	hypothetical prote	936	66.5	4.8	140	2	T21857	hypothetical prote
864	67.5	4.9	665	1	VCMVVR	env polypeptin pr	937	66.5	4.8	243	2	S34794	osmotin - common t
865	67.5	4.9	674	2	T19268	hypothetical prote	938	66.5	4.8	244	1	LNRTMC	mannose-binding le
866	67.5	4.9	771	2	S35681	ESG protein - mous	939	66.5	4.8	251	2	G75495	hypothetical prote
867	67.5	4.9	846	1	PNECA	penicillin amidase	940	66.5	4.8	278	2	H87663	hypothetical prote
868	67.5	4.9	850	2	S56015	gastric mucin MUC5	941	66.5	4.8	294	2	G72706	hypothetical prote
869	67.5	4.9	861	2	A48825	Notch homolog Motc	942	66.5	4.8	301	2	T23441	hypothetical prote
870	67.5	4.9	977	2	I52657	seizure-related pr	943	66.5	4.8	303	2	E90444	conserved hypothet
871	67.5	4.9	1010	2	T36383	probable large ATP	944	66.5	4.8	304	2	T22482	hypothetical prote
872	67.5	4.9	1091	1	PL0009	complement C3d/Eps	945	66.5	4.8	316	2	T19291	hypothetical prote
873	67.5	4.9	1208	2	T27822	hypothetical prote	946	66.5	4.8	337	2	S55932	NCA3 protein precu
874	67.5	4.9	1242	1	DJBEC1	DNA-directed DNA p	947	66.5	4.8	345	2	AH0350	probable DNA-bindi
875	67.5	4.9	1373	2	JE0095	gastric mucin MUC5	948	66.5	4.8	377	2	JC7535	chitinase (EC 3.2.
876	67.5	4.9	1574	2	T13954	MEGF6 protein - ra	949	66.5	4.8	388	2	JC6164	circumsporozoite p
877	67.5	4.9	1706	1	OYBRC	cyclolysin - Borde	950	66.5	4.8	417	2	T08724	hypothetical prote
878	67.5	4.9	1810	1	A32230	tenascin precursor	951	66.5	4.8	428	2	T19309	hypothetical prote
879	67.5	4.9	1838	1	CGHU1V	collagen alpha 1(V	952	66.5	4.8	506	2	F83547	sodium/proline sym
880	67.5	4.9	1843	2	S18803	collagen alpha 1(V	953	66.5	4.8	560	2	H70466	serine proteinase
881	67.5	4.9	2531	2	T31070	notch homolog - se	954	66.5	4.8	576	2	T38293	hypothetical serin
882	67.5	4.9	2531	2	A46019	notch-1 protein -	955	66.5	4.8	589	2	S66856	probable membrane
883	67.5	4.9	6642	2	T29757	protein UNC-89 - C	956	66.5	4.8	589	2	S50355	alpha-glucosidase
884	67	4.9	133	2	H84217	hypothetical prote	957	66.5	4.8	598	2	S65770	maltooligosyltreha
885	67	4.9	163	1	A34313	antifreeze protein	958	66.5	4.8	660	2	S71949	metalloproteinase
886	67	4.9	171	1	JBAO41	chorion class B pr	959	66.5	4.8	673	2	A48089	growth arrest-spec
887	67	4.9	183	2	PN0109	keratin-like prote	960	66.5	4.8	675	2	S20819	collagen alpha 3(I
888	67	4.9	239	2	S07406	thaumatin homolog	961	66.5	4.8	685	2	JC7570	Delta-4 protein -
889	67	4.9	253	2	S49158	complement protein	962	66.5	4.8	688	2	E86409	hypothetical prote
890	67	4.9	264	2	S73040	hypothetical prote	963	66.5	4.8	742	2	JC7595	scavenger receptor
891	67	4.9	272	2	S57460	cytochrome-c oxida	964	66.5	4.8	751	2	S64741	cuticle collagen -
892	67	4.9	299	2	A47031	bialaphos acetylhy	965	66.5	4.8	828	2	G82583	bifunctional aspar
893	67	4.9	327	2	T32164	hypothetical prote	966	66.5	4.8	1085	2	T18369	K-Cl cotransport p
894	67	4.9	336	2	H81091	probable CDP-6-deo	967	66.5	4.8	1085	2	T31429	K-Cl cotransport p
895	67	4.9	343	2	JQ2372	hemagglutinin - in	968	66.5	4.8	1086	2	T14114	K-Cl cotransport p
896	67	4.9	343	2	JQ2371	hemagglutinin - in	969	66.5	4.8	1091	2	A58532	glial cell membran
897	67	4.9	344	2	PQ0321	hemagglutinin - in	970	66.5	4.8	1125	1	OYURCP	speract receptor p
898	67	4.9	344	2	E75621	hemagglutinin - in	971	66.5	4.8	125	2	S45306	notch 3 protein -
899	67	4.9	378	2	JQ1643	probable chromosom	972	66.5	4.8	2318	2	A49128	cell-fate determin
900	67	4.9	401	2	AF3341	precorrin-6y c5,15	973	66.5	4.8	2471	2	A24420	notch protein - fr
901	67	4.9	404	2	T44281	iron-sulfur cofact	974	66.5	4.8	2703	1	UIBO	thyroglobulin prec
902	67	4.9	427	2	T20800	hypothetical prote	975	66.5	4.8	2769	1	AS4849	collagen alpha 1(V
903	67	4.9	456	2	D84651	hypothetical prote	976	66.5	4.8	2944	2	S18252	heparan sulfate pr
904	67	4.9	466	2	C42360	cellulase (EC 3.2.	977	66	4.8	3707	2	AG1960	hypothetical prote
905	67	4.9	566	1	HMIVD1	hemagglutinin prec	978	66	4.8	170	2	AC0689	alternative bacter

979	66	4.8	238	1	LNRTMA	mannose-binding le	1052	65.5	4.8	1629	2	C84839	ferredoxin-depende
980	66	4.8	239	2	D82727	6-phosphogluconola	1053	65.5	4.8	2518	2	AI2140	polyketide synthas
981	66	4.8	256	2	AE0997	probable biotin bi	1054	65.5	4.8	2823	2	F87908	protein T22A3.8 [I
982	66	4.8	306	2	T21938	hypothetical prote	1055	65.5	4.8	2823	2	T23064	hypothetical prote
983	66	4.8	307	2	T18846	hypothetical prote	1056	65.5	4.8	3102	2	T43291	laminin alpha chai
984	66	4.8	311	2	S48400	carrier protein FL	1057	65.5	4.8	3871	2	T22812	hypothetical prote
985	66	4.8	313	2	A35122	metalloproteinase	1058	65.5	4.8	4848	2	T30289	pristinamycin I sy
986	66	4.8	326	2	JQ1437	hemagglutinin - in	1059	65	4.7	111	2	B82830	hypothetical prote
987	66	4.8	336	2	S41643	syrm protein - Rhi	1060	65	4.7	162	2	T49957	ribosomal protein
988	66	4.8	344	2	PQ0319	hemagglutinin - in	1061	65	4.7	181	2	T07661	maturation protein
989	66	4.8	348	2	T29288	hypothetical prote	1062	65	4.7	188	2	A54270	insulin-like growt
990	66	4.8	353	2	D96596	hypothetical prote	1063	65	4.7	188	2	B54270	insulin-like growt
991	66	4.8	355	1	S37460	glutamyl endopepti	1064	65	4.7	229	1	S19713	nitrite hydratase
992	66	4.8	435	2	T15143	hypothetical prote	1065	65	4.7	232	2	E70789	probable protease -
993	66	4.8	553	2	T52362	hypothetical prote	1066	65	4.7	249	2	F70925	hypothetical prote
994	66	4.8	614	2	T06741	hypothetical prote	1067	65	4.7	287	2	D70625	probable transposa
995	66	4.8	687	2	T02459	probable beta-amyl	1068	65	4.7	299	2	T20605	hypothetical prote
996	66	4.8	753	2	S35371	finger protein neu	1069	65	4.7	303	2	S45461	hypothetical prote
997	66	4.8	787	2	T05617	hypothetical prote	1070	65	4.7	311	2	F75366	hypothetical prote
998	66	4.8	854	2	A96574	protein F12M16.30	1071	65	4.7	313	2	H89865	hypothetical prote
999	66	4.8	864	2	T30441	probable capsid-as	1072	65	4.7	313	2	T22828	hypothetical prote
1000	66	4.8	1194	2	C59436	KIAA1391 protein [	1073	65	4.7	342	2	A46396	ets-related protei
1001	66	4.8	1964	2	T09059	notch4 - mouse	1074	65	4.7	349	2	T43457	hypothetical prote
1002	66	4.8	2114	2	E96505	hypothetical prote	1075	65	4.7	356	2	T22827	hypothetical prote
1003	66	4.8	2193	2	S52919	polypeptide (1A, 1	1076	65	4.7	358	2	T36415	probable iron-side
1004	66	4.8	3442	2	E82589	hemagglutinin-like	1077	65	4.7	359	1	S28043	cinnamyl-alcohol d
1005	66	4.8	3455	2	B82519	hemagglutinin-like	1078	65	4.7	370	2	T22510	hypothetical prote
1006	66	4.8	3507	2	T34513	hypothetical prote	1079	65	4.7	406	2	S73592	glycine hydroxymet
1007	65.5	4.8	37	2	S03570	trypsin (EC 3.4.21	1080	65	4.7	416	2	H82968	sarcosine oxidase
1008	65.5	4.8	97	2	S26898	Ig heavy chain V r	1081	65	4.7	418	2	T34606	probable fumarylac
1009	65.5	4.8	97	2	JH0428	Ig gamma chain V r	1082	65	4.7	428	2	D83861	hypothetical prote
1010	65.5	4.8	114	2	I72667	cold agglutinin FS	1083	65	4.7	446	2	T10711	anthranilate N-ben
1011	65.5	4.8	117	2	T35913	hypothetical prote	1084	65	4.7	469	2	T36362	probable DNA repai
1012	65.5	4.8	140	2	S78052	Ig heavy chain pre	1085	65	4.7	476	2	T29054	probable transmemb
1013	65.5	4.8	147	2	A84546	50S ribosomal prot	1086	65	4.7	619	2	T08613	hypothetical prote
1014	65.5	4.8	202	2	T35703	hypothetical prote	1087	65	4.7	711	2	D86296	hypothetical prote
1015	65.5	4.8	228	2	T49891	glycine-rich prote	1088	65	4.7	711	2	S05381	VGf8a protein prec
1016	65.5	4.8	245	1	ClHUQA	complement subcomp	1089	65	4.7	715	2	S52675	probable membrane
1017	65.5	4.8	286	2	F71524	dihydrodipicolinat	1090	65	4.7	737	2	T02178	hypothetical prote
1018	65.5	4.8	298	2	T27644	hypothetical prote	1091	65	4.7	759	2	T44142	DR1 protein [impor
1019	65.5	4.8	304	2	JC5845	chitinase (EC 3.2.	1092	65	4.7	783	2	T35389	probable serine-th
1020	65.5	4.8	311	2	E85867	hypothetical prote	1093	65	4.7	784	2	JQ0317	hypothetical 82K p
1021	65.5	4.8	311	2	D91023	hypothetical prote	1094	65	4.7	826	2	A60385	monocyte surface a
1022	65.5	4.8	327	2	AG3367	alcohol dehydrogen	1095	65	4.7	837	2	E70835	hypothetical glyci
1023	65.5	4.8	350	2	S63248	hypothetical prote	1096	65	4.7	866	2	S57936	CotC protein precu
1024	65.5	4.8	360	2	T37285	collagen dpy-2 - C	1097	65	4.7	881	2	T49279	hypothetical prote
1025	65.5	4.8	363	2	T16831	hypothetical prote	1098	65	4.7	984	2	T00326	hypothetical prote
1026	65.5	4.8	371	2	B72461	hypothetical prote	1099	65	4.7	1112	2	S49432	hypothetical prote
1027	65.5	4.8	396	2	T29773	hypothetical prote	1100	65	4.7	1196	1	DNBEKS	DNA-binding protei
1028	65.5	4.8	397	2	S28274	hypothetical prote	1101	65	4.7	1374	2	T16129	hypothetical prote
1029	65.5	4.8	402	1	CGBO2S	collagen alpha 2(I	1102	65	4.7	1439	2	T02087	gag/pol polyprotei
1030	65.5	4.8	452	2	T30082	hypothetical prote	1103	65	4.7	1489	2	D70807	hypothetical glyci
1031	65.5	4.8	467	1	WZBE61	gene 61 protein -	1104	65	4.7	1522	2	T00028	brain-specific ang
1032	65.5	4.8	479	2	C90457	cytochrome b558/56	1105	65	4.7	1603	1	BVASA1	3-dehydroquinat s
1033	65.5	4.8	488	2	A27353	collagen alpha 1(I	1106	65	4.7	1707	2	A33526	collagen alpha 2(I
1034	65.5	4.8	576	2	S33327	catalase (EC 1.11.	1107	65	4.7	1901	2	F70806	CRP-ductin-alpha p
1035	65.5	4.8	615	2	A05269	collagen alpha 1(I	1108	65	4.7	2083	2	T42721	calcium channel pr
1036	65.5	4.8	691	2	A54741	erythrocyte membra	1109	65	4.7	2166	2	S11339	calcium channel al
1037	65.5	4.8	730	2	A36226	collagen alpha 1 c	1110	65	4.7	2171	2	S05054	RNA-directed RNA p
1038	65.5	4.8	741	2	G69514	hypothetical prote	1111	65	4.7	2244	2	T08212	protein-tyrosine-p
1039	65.5	4.8	775	2	A61228	collagen alpha 2(I	1112	65	4.7	2294	2	I67630	surface protein ty
1040	65.5	4.8	782	2	B83966	formate dehydrogen	1113	65	4.7	2395	1	S50820	protein-tyrosine-p
1041	65.5	4.8	877	2	T03098	p97 protein - Toxo	1114	65	4.7	2466	2	I67629	protein-tyrosine-p
1042	65.5	4.8	947	2	T23107	hypothetical prote	1115	65	4.7	2490	1	A54971	protein-tyrosine-p
1043	65.5	4.8	966	1	P1BVB	RNA 1a protein - b	1116	65	4.7	2509	2	G01880	fatty-acid synthas
1044	65.5	4.8	969	2	B87083	exonuclease ABC s	1117	64.5	4.7	159	2	I49618	gamma-F-crystallin
1045	65.5	4.8	1137	2	T02097	glutamate synthase	1118	64.5	4.7	171	2	A34493	collagen alpha 1(I
1046	65.5	4.8	1210	1	GQHUE	epidermal growth f	1119	64.5	4.7	191	2	D90712	lipoate biosynthes
1047	65.5	4.8	1295	2	A32901	glp1 protein precu	1120	64.5	4.7	191	2	H85562	lipoate biosynthes
1048	65.5	4.8	1353	1	JQ2168	E2 glycoprotein pr	1121	64.5	4.7	191	2	D64797	lipoate-protein li
1049	65.5	4.8	1360	2	T33922	hypothetical prote	1122	64.5	4.7	210	2	T20973	hypothetical prote
1050	65.5	4.8	1376	1	JQ1534	E2 glycoprotein pr	1123	64.5	4.7	222	2	A88102	protein W09G10.1 [
1051	65.5	4.8	1492	2	A40333	collagen alpha 1'(	1124	64.5	4.7	232	2	E90834	minor tail protein



1125	64.5	4.7	242	2	S60143	cellulase (EC 3.2.
1126	64.5	4.7	262	2	A54889	IgE-binding protei
1127	64.5	4.7	266	2	T22706	hypothetical prote
1128	64.5	4.7	277	1	QBEC2	HKRFX protein - hu
1129	64.5	4.7	297	2	T27525	hypothetical prote
1130	64.5	4.7	301	2	B31219	collagen 2 - Caeno
1131	64.5	4.7	317	2	T29960	hypothetical prote
1132	64.5	4.7	318	2	S27977	cuticle collagen d
1133	64.5	4.7	328	2	AD1916	alcohol dehydrogen
1134	64.5	4.7	333	2	T15867	hypothetical prote
1135	64.5	4.7	354	2	B75400	phosphoribosylform
1136	64.5	4.7	356	2	T05119	leucoanthocyanidin
1137	64.5	4.7	387	2	E95933	probable calcium-b
1138	64.5	4.7	398	2	B71284	probable periplasm
1139	64.5	4.7	411	2	B91220	probable arylsulfa
1140	64.5	4.7	411	2	D86066	probable arylsulfa
1141	64.5	4.7	411	2	S58105	Cu metalloregulato
1142	64.5	4.7	416	2	T41665	probable dipeptida
1143	64.5	4.7	445	2	D86620	phosphoshikimate v
1144	64.5	4.7	445	2	D86620	phosphoshikimate v
1145	64.5	4.7	460	1	QORT	hemopexin precursor
1146	64.5	4.7	529	2	S36578	Li protein - human
1147	64.5	4.7	532	2	AE1964	Dnak-type molecula
1148	64.5	4.7	547	1	A32244	60K cysteine-rich
1149	64.5	4.7	553	2	D71515	60K cysteine-rich
1150	64.5	4.7	562	2	A85524	choline dehydrogen
1151	64.5	4.7	562	2	E90673	choline dehydrogen
1152	64.5	4.7	570	2	S42708	proline transport
1153	64.5	4.7	570	2	S04547	proline transport
1154	64.5	4.7	597	2	JC7615	alpha-glucosidase
1155	64.5	4.7	599	2	T25835	hypothetical prote
1156	64.5	4.7	618	2	S32436	collagen alpha 2(I
1157	64.5	4.7	626	2	C72035	succinate dehydrog
1158	64.5	4.7	626	2	C86589	succinate dehydrog
1159	64.5	4.7	644	2	JC2346	kexin-like protein
1160	64.5	4.7	646	2	H96665	protein F22C12.10
1161	64.5	4.7	653	1	S23667	cytochrome c-type
1162	64.5	4.7	653	2	T02080	probable carbonate
1163	64.5	4.7	666	2	F71310	probable periplasm
1164	64.5	4.7	678	2	B84856	hypothetical prote
1165	64.5	4.7	715	2	S70397	zona pellucida gly
1166	64.5	4.7	721	2	C84732	probable homeodoma
1167	64.5	4.7	724	2	C71274	hypothetical prote
1168	64.5	4.7	730	2	H86295	hypothetical prote
1169	64.5	4.7	884	2	S61569	hypothetical prote
1170	64.5	4.7	1374	1	GNNYEC	genome polypeptid
1171	64.5	4.7	1376	1	VGIHJ2	E2 glycoprotein pr
1172	64.5	4.7	1388	2	A53317	collagen alpha 1(X
1173	64.5	4.7	1408	2	S16148	gene serrate prote
1174	64.5	4.7	1487	2	T02850	hypothetical prote
1175	64.5	4.7	1546	1	CGHU2E	collagen alpha 2(X
1176	64.5	4.7	1712	1	CGHU2B	collagen alpha 2(I
1177	64.5	4.7	2139	2	A35672	crumbs protein - f
1178	64.5	4.7	3623	2	T09456	intrinsic factor-B
1179	64	4.7	104	2	JH0345	T-cell receptor al
1180	64	4.7	118	1	A31429	hisactophilin [val
1181	64	4.7	128	2	JQ1002	keratin, claw - ch
1182	64	4.7	133	2	B38911	Ig heavy chain V r
1183	64	4.7	218	2	T03287	osmotin protein ho
1184	64	4.7	238	2	B75266	phosphoribosylform
1185	64	4.7	248	1	LNHUP6	pulmonary surfacta
1186	64	4.7	278	2	C43670	integral membrane
1187	64	4.7	304	2	T23801	hypothetical prote
1188	64	4.7	310	2	T29731	hypothetical prote
1189	64	4.7	333	2	T50630	hypothetical prote
1190	64	4.7	346	2	T45069	8-hydroxy-guanine
1191	64	4.7	394	1	VGBE17	glycoprotein D pr
1192	64	4.7	394	1	VGBED1	glycoprotein D - h
1193	64	4.7	401	2	C89102	protein F25E5.10 l
1194	64	4.7	411	2	T16982	glutamate dehydrog
1195	64	4.7	411	2	T04342	glutamate dehydrog
1196	64	4.7	411	2	T03294	glutamate dehydrog
1197	64	4.7	426	2	AH2144	hypothetical prote

1198	64	4.7	426	2	D88103	protein W10G11.6 l
1199	64	4.7	465	1	S47738	cytochrome-c perox
1200	64	4.7	465	2	F91178	cytochrome-c perox
1201	64	4.7	465	2	G86024	cytochrome-c perox
1202	64	4.7	487	2	T45923	hypothetical prote
1203	64	4.7	502	2	S36526	Li protein - human
1204	64	4.7	504	2	S56745	mucin (clone pGM31
1205	64	4.7	516	2	S42093	cellulose 1,4-beta
1206	64	4.7	566	1	HMIVUR	hemagglutinin prec
1207	64	4.7	566	2	S69888	hemagglutinin prec
1208	64	4.7	595	2	F95379	probable adenine d
1209	64	4.7	663	1	S18572	tetracycline resis
1210	64	4.7	669	2	A35103	cell surface recep
1211	64	4.7	697	2	T37946	tryptophan synthas
1212	64	4.7	717	2	T49238	hypothetical prote
1213	64	4.7	719	2	A87292	primosomal protein
1214	64	4.7	721	2	F70649	probable Acyl-CoA
1215	64	4.7	728	2	I50719	C-Delta-1 - chicke
1216	64	4.7	753	2	AH0097	probable biotin su
1217	64	4.7	823	2	T21104	hypothetical prote
1218	64	4.7	843	2	T13334	probable tail-host
1219	64	4.7	861	2	B49847	nitrate reductase
1220	64	4.7	895	2	AD0541	outer membrane fim
1221	64	4.7	963	2	T19140	hypothetical prote
1222	64	4.7	998	2	T35745	probable ATP-bindi
1223	64	4.7	1000	2	AB3467	sarcosine oxidase
1224	64	4.7	1083	2	H86921	probable arabinosy
1225	64	4.7	1955	1	AGCH	agrin precursor -
1226	64	4.7	2042	2	T18399	variant-specific s
1227	64	4.7	2321	2	S78549	notch3 protein - h
1228	64	4.7	3137	2	A37797	collagen alpha 3(V
1229	64	4.7	3461	2	S58870	reelin precursor -
1230	64	4.7	3635	2	T10053	laminin alpha 5 ch
1231	64	4.7	7463	2	T36248	CDA peptide synthe
1232	63.5	4.6	97	2	G34964	Ig heavy chain V-I
1233	63.5	4.6	144	2	S24805	hypothetical prote
1234	63.5	4.6	152	2	T24064	hypothetical prote
1235	63.5	4.6	184	2	D83234	hypothetical prote
1236	63.5	4.6	191	2	I46412	keratin KAP5.4 - s
1237	63.5	4.6	191	2	AF0580	lipote-protein li
1238	63.5	4.6	215	2	AD0455	thiamine-phosphate
1239	63.5	4.6	220	2	S35789	US2 protein - bovi
1240	63.5	4.6	232	1	TLBPLL	minor tail protein
1241	63.5	4.6	234	2	T31753	hypothetical prote
1242	63.5	4.6	253	1	C1HUQB	complement subcomp
1243	63.5	4.6	256	2	T28853	hypothetical prote
1244	63.5	4.6	269	2	C83516	hypothetical prote
1245	63.5	4.6	281	2	T32765	hypothetical prote
1246	63.5	4.6	281	2	C88638	protein F58F6.1 [i
1247	63.5	4.6	289	2	T34241	hypothetical prote
1248	63.5	4.6	289	2	T26812	hypothetical prote
1249	63.5	4.6	290	2	A32249	collagen - sea urc
1250	63.5	4.6	291	2	T34494	hypothetical prote
1251	63.5	4.6	294	2	T23916	hypothetical prote
1252	63.5	4.6	308	2	H90452	conserved hypothet
1253	63.5	4.6	311	2	B64998	hypothetical prote
1254	63.5	4.6	316	2	T20497	hypothetical prote
1255	63.5	4.6	320	2	C81029	3-oxoacyl-(acyl-ca
1256	63.5	4.6	320	2	T39110	probable gtpase ac
1257	63.5	4.6	326	2	T02340	GTP-binding regula
1258	63.5	4.6	328	2	T16970	GTP-binding protei
1259	63.5	4.6	335	2	A40038	MHC class I histoc
1260	63.5	4.6	338	2	T49182	probable chloropla
1261	63.5	4.6	357	2	H75541	probable oxidoredu
1262	63.5	4.6	371	2	E88633	protein F56B3.1 [i
1263	63.5	4.6	375	2	A95867	probable pyrroloqu
1264	63.5	4.6	378	2	AB0894	conserved hypothet
1265	63.5	4.6	381	2	T27806	hypothetical prote
1266	63.5	4.6	388	2	T22553	hypothetical prote
1267	63.5	4.6	404	2	T40553	Trp-Asp repeat pro
1268	63.5	4.6	418	2	S31124	hypothetical prote
1269	63.5	4.6	435	2	B87412	conserved hypothet
1270	63.5	4.6	445	2	C72695	probable amidase A

1271 63.5 4.6 481 2 A33712 metalloproteinase  
1272 63.5 4.6 498 2 B84789 probable protein w  
1273 63.5 4.6 504 1 P1WL31 L1 protein - human  
1274 63.5 4.6 538 2 S65764 chitinase (EC 3.2.  
1275 63.5 4.6 556 1 S10901 choline dehydrogen  
1276 63.5 4.6 654 2 A34734 transcription fact  
1277 63.5 4.6 660 2 C90343 conserved hypothet  
1278 63.5 4.6 680 2 T25832 hypothetical prote  
1279 63.5 4.6 690 2 T08604 hypothetical prote  
1280 63.5 4.6 700 2 T41401 spore outgrowth fa  
1281 63.5 4.6 724 2 D87530 isoquinoline 1-oxi  
1282 63.5 4.6 728 2 S26427 70K structural pro  
1283 63.5 4.6 742 4 C34734 transcription fact  
1284 63.5 4.6 768 2 A42755 P-selectin precurs  
1285 63.5 4.6 803 2 C83561 probable type II s  
1286 63.5 4.6 825 4 B34734 transcription fact  
1287 63.5 4.6 872 2 S49538 Cooc protein precu  
1288 63.5 4.6 883 2 T07651 potassium channel  
1289 63.5 4.6 901 2 T04108 receptor kinase ho  
1290 63.5 4.6 907 2 T15792 hypothetical prote  
1291 63.5 4.6 932 2 I52527 PACE4A - mouse (fr  
1292 63.5 4.6 1042 2 T26644 hypothetical prote  
1293 63.5 4.6 1345 2 S46817 hypothetical prote  
1294 63.5 4.6 1381 2 E70806 hypothetical Glyci  
1295 63.5 4.6 1549 2 I48103 type VII collagen  
1296 63.5 4.6 1573 2 S01845 DNA (cytosine-5)-  
1297 63.5 4.6 1649 2 C86822 hypothetical prote  
1298 63.5 4.6 1693 2 S76086 beta transducin-li  
1299 63.5 4.6 1959 1 AGRT agrin - rat  
1300 63.5 4.6 2185 1 GNNYBT genome polyprotein  
1301 63.5 4.6 2185 1 JQ2021 genome polyprotein  
1302 63.5 4.6 2195 2 T34264 hypothetical prote  
1303 63.5 4.6 2352 2 T30201 Notch homolog prot  
1304 63.5 4.6 2533 2 T28675 alpha-51D immobili  
1305 63.5 4.6 2533 2 T28674 alpha-51D-immobili  
1306 63.5 4.6 3063 2 S55505 fatty-acid synthas  
1307 63.5 4.6 3429 2 T13853 hypothetical prote  
1308 63 4.6 40 2 A49081 capillary permeabi  
1309 63 4.6 99 2 S26801 Ig heavy chain V r  
1310 63 4.6 119 2 B45937 early chorion prot  
1311 63 4.6 119 2 S24294 chorion protein -  
1312 63 4.6 198 2 A83153 hypothetical prote  
1313 63 4.6 212 2 E86179 hypothetical prote  
1314 63 4.6 228 2 A44982 collagen UCOL1 - p  
1315 63 4.6 240 2 F70631 probable sodC prot  
1316 63 4.6 242 1 F75433 probable phosphoes  
1317 63 4.6 245 1 C1HUQC complement subcomp  
1318 63 4.6 248 1 LNHUPS pulmonary surfacta  
1319 63 4.6 257 2 T28946 hypothetical prote  
1320 63 4.6 265 2 AG0814 cob(I)alamin adeno  
1321 63 4.6 269 2 S36166 paired box transcr  
1322 63 4.6 285 2 T29982 hypothetical prote  
1323 63 4.6 299 2 T24833 hypothetical prote  
1324 63 4.6 302 2 T15936 hypothetical prote  
1325 63 4.6 303 2 E86591 CT580 hypothetical  
1326 63 4.6 303 2 D72031 ct580 hypothetical  
1327 63 4.6 308 2 S32172 neurosporene hydro  
1328 63 4.6 309 2 H69995 hypothetical prote  
1329 63 4.6 320 2 C81972 probable 3-oxoacyl  
1330 63 4.6 326 2 JS0169 collagen col-14 -  
1331 63 4.6 348 2 T28623 hypothetical prote  
1332 63 4.6 349 2 D36858 gene G4R protein -  
1333 63 4.6 357 1 S33321 glutamyl endopepti  
1334 63 4.6 369 2 S33603 surfactant protein  
1335 63 4.6 383 2 A83518 hypothetical prote  
1336 63 4.6 400 2 C75336 serine proteinase,  
1337 63 4.6 403 2 H98327 enantiomer-selecti  
1338 63 4.6 418 2 T15142 hypothetical prote  
1339 63 4.6 422 1 A56674 paired box transcr  
1340 63 4.6 424 2 C86247 hypothetical prote  
1341 63 4.6 428 2 T27544 zinc resistance pr  
1342 63 4.6 434 2 D96760 hypothetical prote  
1343 63 4.6 436 1 S42234 paired box transcr

1344 63 4.6 437 2 JC7138 alpha-amylase (EC  
1345 63 4.6 437 2 JT0946 alpha-amylase 3E -  
1346 63 4.6 438 2 D88206 protein nhr-21.a l  
1347 63 4.6 453 2 A71891 glu-tRNA amidotran  
1348 63 4.6 453 2 AF2955 glutamyl-tRNA amid  
1349 63 4.6 471 2 A39024 collagen alpha 3(I  
1350 63 4.6 475 2 AB0855 conserved hypothet  
1351 63 4.6 475 2 H91077 probable 4-hydroxy  
1352 63 4.6 475 2 T44997 probable 4-hydroxy  
1353 63 4.6 475 2 A85923 probable 4-hydroxy  
1354 63 4.6 480 2 F70785 hypothetical prote  
1355 63 4.6 487 2 T21384 hypothetical prote  
1356 63 4.6 513 1 EUTQI cellulose 1,4-beta  
1357 63 4.6 513 2 S45380 cellulose 1,4-beta  
1358 63 4.6 543 2 H82282 vibriobactin-speci  
1359 63 4.6 545 2 T02079 probable carbonate  
1360 63 4.6 582 2 S10099 transcription fact  
1361 63 4.6 611 2 T27013 hypothetical prote  
1362 63 4.6 622 2 T27155 hypothetical prote  
1363 63 4.6 633 2 B40983 collagen alpha 1(X  
1364 63 4.6 638 2 I53169 cyokeratin 2 - hu  
1365 63 4.6 658 2 AB3253 glucose inhibited  
1366 63 4.6 684 2 F83375 hypothetical prote  
1367 63 4.6 692 2 B69628 translation elonga  
1368 63 4.6 692 2 T44380 translation elonga  
1369 63 4.6 695 2 AE1406 translation elonga  
1370 63 4.6 695 2 AE1782 translation elonga  
1371 63 4.6 695 2 G87316 nuclease, probable  
1372 63 4.6 705 2 C84406 hypothetical prote  
1373 63 4.6 760 2 A45174 eye cell developme  
1374 63 4.6 946 2 T16297 hypothetical prote  
1375 63 4.6 1125 1 S57846 protein-tyrosine k  
1376 63 4.6 1170 2 A53612 laminin Blk chain  
1377 63 4.6 1203 2 A49175 Motch B protein -  
1378 63 4.6 1331 2 T18310 receptor-adenylate  
1379 63 4.6 1345 2 S55669 tegument protein 7  
1380 63 4.6 1367 2 T33819 hypothetical prote  
1381 63 4.6 1820 2 A55494 latent transformin  
1382 63 4.6 2157 1 GNNY1B genome polyprotein  
1383 63 4.6 2437 2 S42612 transmembrane prot  
1384 63 4.6 2647 2 A37098 gelation factor AB  
1385 63 4.6 3176 2 CGH3A collagen alpha 3(V  
1386 62.5 4.5 97 2 S14474 Ig heavy chain V r  
1387 62.5 4.5 118 2 S29653 textilotoxin chain  
1388 62.5 4.5 144 2 S01391 phospholipase A2 (  
1389 62.5 4.5 155 2 C44012 insulin-like growt  
1390 62.5 4.5 165 2 S72776 B1496\_F1\_41 protei  
1391 62.5 4.5 181 2 A70627 hypothetical prote  
1392 62.5 4.5 198 2 I49558 collagen alpha 1(I  
1393 62.5 4.5 214 2 T18539 phosphoglycerate m  
1394 62.5 4.5 222 2 S19931 glycine-rich prote  
1395 62.5 4.5 231 2 B23746 Ig Fab region IV-J  
1396 62.5 4.5 247 2 S33197 osmotin-like prote  
1397 62.5 4.5 299 2 T29956 hypothetical prote  
1398 62.5 4.5 306 2 H81036 riboflavin kinase/  
1399 62.5 4.5 313 2 T33010 hypothetical prote  
1400 62.5 4.5 316 2 T19288 hypothetical prote  
1401 62.5 4.5 341 2 F70625 hypothetical prote  
1402 62.5 4.5 352 2 JE0296 thyrotropin releas  
1403 62.5 4.5 356 2 S61061 hypothetical prote  
1404 62.5 4.5 359 2 T22774 hypothetical prote  
1405 62.5 4.5 391 2 F87258 acyl-CoA dehydroge  
1406 62.5 4.5 398 2 AG0128 1-deoxy-D-xylulose  
1407 62.5 4.5 398 2 T35255 probable racemase  
1408 62.5 4.5 402 2 S37789 hypothetical prote  
1409 62.5 4.5 411 2 S71217 glutamate dehydrog  
1410 62.5 4.5 427 2 S75210 glycine hydroxymet  
1411 62.5 4.5 450 2 E70681 probable trpE - My  
1412 62.5 4.5 466 2 A87638 glutamate-1-semial  
1413 62.5 4.5 473 2 A56175 adhesive plaque pr  
1414 62.5 4.5 478 2 S31906 beta-1,3-glucanase  
1415 62.5 4.5 482 2 S76376 hypothetical prote









Qy	59	TAHCGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPV	118
Db	60	SAAHCKYRIQVRLGEHNINVLGNEQFVDSAKIIRHPNY--NSWTLNDNDIMLIKLASPV	117
Qy	119	RVTSVQPLPLPNDCATAGTECHVSGWG--ITNHPRNPFDDLQCLNLSIVSHATCHGVY	176
Db	118	TLNARVASVPLPSSCAPAGTQCLISGWGNTLSNGVNN--PDLLQCVDAFVLPQADCEASY	175
Qy	177	PGRITSNMVCAGGVP-GQDACQDGGGPLVCGVLQGLVSWGSGVPCGQDGIPGVYTYIC	235
Db	176	PGDITNMICVGFLEGGKDSQCGDSGGPVVVCNGELQGIIVSWG--GCAQPDAPGVYTKVC	233
Qy	236	KYVDWIRMIMRNN	248
Db	234	NYVDWIQNTIADN	246
RESULT 8			
TREOTR			
N;Contains: trypsinogen			
C;Species: Bos primigenius taurus (cattle)			
C;Date: 24-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 18-Jul-1997			
C;Accession: A90164; A00946; S08774			
R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.			
Biochem. Biophys. Res. Commun. 24, 346-352, 1966			
A;Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.			
A;Reference number: A90164; MUID:67168848; PMID:5967094			
A;Accession: A90164			
A;Molecule type: protein			
A;Residues: 1-57,'Q',59-67,'Q',69-150,'N',152-176,'N',178-229 <MIK>			
R;Hartley, B.S.			
Philos. Trans. R. Soc. Lond. B257, 77-87, 1970			
A;Reference number: A93755			
A;Contents: annotation; revisions			
R;Titani, K.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.			
Biochemistry 14, 1358-1366, 1975			
A;Title: Amino acid sequence of dogfish trypsin.			
A;Reference number: A00950; MUID:75146445; PMID:1092332			
A;Contents: annotation; revisions			
A;Note: the sequence agrees with that shown			
R;Bode, W.; Schwager, P.			
J. Mol. Biol. 98, 693-717, 1975			
A;Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution.			
A;Reference number: A92954; MUID:76072097; PMID:512			
A;Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and			
C;Comment: Trypsinogen is synthesized in the acinar cells of the pancreas.			
C;Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a termi			
s,pseudotrypsin. A cleavage may also occur after Arg-105.			
C;Superfamily: trypsin; trypsin homology			
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen			
F;1-229/Product: trypsinogen #status experimental <ZYM>			
F;1-6/Domain: activation peptide #status experimental <APT>			
F;7-222/Domain: trypsin homology <TRY>			
F;7-131,132-229/Product: alpha-trypsin #status experimental <MPT>			
F;6-7/Cleavage site: Lys-Ile (enteropeptidase) #status experimental			
F;13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental			
F;46,90,183/Active site: His, Asp, Ser #status experimental			
F;58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental			
F;131-132/Cleavage site: Lys-Ser (autolytic) #status experimental			
Query Match 40.2%; Score 552; DB 1; Length 229;			
Best Local Similarity 46.3%; Pred. No. 1.4e-37;			
Matches 106; Conservative 40; Mismatches 77; Indels 6; Gaps 4;			
Qy	21	KIFNGTECGRNSQPWQVGLFEGLSLRCGGVLIDHRVLTAAHCSGRYWVRLGEHSLSQL	80
Db	6	KIVGYTCGANTVPYQVSLNSGYHF-CGGSLLNSQWTVVSAHCYKSGIQVRLGEDNINWV	64
Qy	81	DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSVQPLPLPNDCATAGTEC	140
Db	65	EGNEQFISAKSIVHPSY--NSNTLNNDIMLIKLSAASLSNRVASISLPTSCASAGTQC	122

Qy	141	HVSGWGITNHPRNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD	199
Db	123	LISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSQGD	182
Qy	200	SGGPLVCGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN	248
Db	183	SGGPVVCSGKLQGIIVSWG--GCAQKNKPGVYTKVCNYVSWIKQTIASN	229
RESULT 9			
S13813			
trypsin (EC 3.4.21.4) - bovine			
C;Species: Bos primigenius taurus (cattle)			
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004			
C;Accession: S13813			
R;le Huerou, I.; Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.			
Eur. J. Biochem. 193, 767-773, 1990			
A;Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anionic tr			
A;Reference number: S13813; MUID:91065383; PMID:1701147			
A;Accession: S13813			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-247 <HUE>			
A;Cross-references: UNIPROT:Q29463; EMBL:X54703; NID:g829; PIDN:CAA38513.1; PID:g830			
C;Superfamily: trypsin; trypsin homology			
C;Keywords: hydrolase; protein digestion; serine proteinase			
F;24-239/Domain: trypsin homology <TRY>			
F;63,107,200/Active site: His, Asp, Ser #status predicted			
Query Match 40.0%; Score 550; DB 2; Length 247;			
Best Local Similarity 45.7%; Pred. No. 2.3e-37;			
Matches 113; Conservative 40; Mismatches 84; Indels 10; Gaps 5;			
Qy	7	LLLCVLGLSQA---ATPKIFNGTECGRNSQPWQVGLFEGLSLRCGGVLIDHRWVLTAAH	62
Db	5	LILAFVGAAVAFPSDDDDKIVGGYTCAESVPYQVSLNAGYHF-CGGSLLNDQWVVSAAH	63
Qy	63	CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTS	122
Db	64	CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLNDNDILLIKLSTPAVINA	121
Qy	123	SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFDDLQCLNLSIVSHATCHGVYPGRITS	182
Db	122	RVSTILLPSACASAGTECLISGWNTLSSGVNYPDLLQCLVAPLLSHADCEASYPGQITN	181
Qy	183	NMVCAGGVP-GQDACQDSDGGPLVCGGVQLGLVSWGSGVPCGQDGIPGVYTYICKYVDWI	241
Db	182	NMICAGFLEGGKDSQCGDSGGPVACNGQLQGIIVSWG--GCAQKKGPGVYTKVCNYVDWI	239
Qy	242	RMIMRNN	248
Db	240	QETIAAN	246
RESULT 10			
TRDG			
trypsin (EC 3.4.21.4) precursor, anionic - dog			
N;Alternate names: cationic trypsinogen			
C;Species: Canis lupus familiaris (dog)			
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004			
C;Accession: A26273			
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.			
Mol. Cell. Biol. 5, 2669-2676, 1985			
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque			
A;Reference number: A26273; MUID:86284628; PMID:3841794			
A;Accession: A26273			
A;Molecule type: mRNA			
A;Residues: 1-247 <PIN>			
A;Cross-references: UNIPROT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095			
C;Superfamily: trypsin; trypsin homology			
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen			
F;1-15/Domain: signal sequence #status predicted <SIG>			







OM protein - protein search, using sw model  
Run on: March 5, 2005, 17:55:12 ; Search time 165 Seconds  
(without alignments)  
581.313 Million cell updates/sec

Title: US-10-006-856A-194  
Perfect score: 1374  
Sequence: 1 MGLSIFLLLCVLGSLQAATP.....GVYTYICKYVDWIRMIRNN 248  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

GenCore version 5.1.6  
SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAB21304	standard; protein; 248 AA.				
DE	Human KLX-L5	protein #4.				
PN	WO200053776-A2.					
PD	14-SEP-2000.					
PA	(MOUN ) MOUNT SINAI HOSPITAL.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 2						
ID	AAB24428	standard; protein; 248 AA.				
DE	Human PRO1303	protein sequence SEQ ID NO:203.				
PN	WO200032221-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 3						
ID	AAB24032	standard; protein; 248 AA.				
DE	Human PRO1303	protein sequence SEQ ID NO:33.				
PN	WO200053750-A1.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 4						
ID	AAV93393	standard; protein; 248 AA.				
DE	Human PRO1303	(UNQ669) amino acid sequence SEQ ID NO:194.				
PN	WO200012708-A2.					
PD	09-MAR-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1374;	DB 3;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 5						
ID	AAM23994	standard; protein; 248 AA.				
DE	Human EST encoded	protein SEQ ID NO: 1519.				
PN	WO200154477-A2.					
PD	02-AUG-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1374;	DB 4;	Length 248;		
Best Local Similarity	100.0%;	Pred. No. 5e-98;				
RESULT 6						
ID	AAB66142	standard; protein; 248 AA.				

DE Protein of the invention #54.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 7  
ID ABO33635 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 6; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 8  
ID ABO44488 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 9  
ID ABO33512 standard; protein; 248 AA.  
DE Novel human secreted and transmembrane protein PRO1303.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 10  
ID ADC18063 standard; protein; 248 AA.  
DE Human PRO polypeptide #54.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 11  
ID ADD70709 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 12  
ID ADD39786 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 13  
ID ADD70232 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 14  
ID ADD38353 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 15  
ID ADD39309 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.



PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 16  
ID ADD38832 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 17  
ID ADD40263 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 18  
ID ADE50484 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 19  
ID ADE20096 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 20  
ID ADE50007 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 21  
ID ADE21565 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 22  
ID ADF29990 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 23  
ID ADF55883 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 24  
ID ADH99387 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003065142-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 7; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 25  
ID ADE96567 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 26  
ID ADF25878 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 27  
ID ADF24777 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 28  
ID ADF29513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 29  
ID ADE97044 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 30  
ID ADH03082 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 31  
ID ADH04036 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 32  
ID ADH03559 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 33  
ID ADH04513 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004005626-A1.  
PD 08-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 34  
ID ADH61514 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 35  
ID ADN10927 standard; protein; 248 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 36  
ID ADL94713 standard; protein; 248 AA.  
DE Human secreted/transmembrane protein PRO1303.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 37  
ID ADT94373 standard; protein; 248 AA.  
DE Human PRO1303 protein.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1374; DB 8; Length 248;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
RESULT 38  
ID AAO29516 standard; protein; 248 AA.  
DE Human kallikrein-like protein 5 (18817).  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 99.5%; Score 1367; DB 6; Length 248;  
Best Local Similarity 99.6%; Pred. No. 1.7e-97;  
RESULT 39  
ID AAB21303 standard; protein; 254 AA.  
DE Human KLK-L5 protein #3.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 3; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 40  
ID ABG66676 standard; protein; 254 AA.  
DE Human novel polypeptide #11.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 94.7%; Score 1301; DB 5; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 41  
ID ADN10926 standard; protein; 254 AA.  
DE Human kallikrein 12, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 42  
ID ADP56174 standard; protein; 254 AA.  
DE Human PRO protein sequence SEQ ID NO:2150.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.

Query Match 94.7%; Score 1301; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.2e-92;  
RESULT 43  
ID AAB21301 standard; protein; 184 AA.  
DE Human KLK-L5 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 74.2%; Score 1019; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.5e-71;  
RESULT 44  
ID AAY28642 standard; protein; 162 AA.  
DE Human secreted protein from cDNA clone HKAFV61.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 59.0%; Score 811; DB 2; Length 162;  
Best Local Similarity 64.1%; Pred. No. 8.1e-55;  
RESULT 45  
ID AAY32852 standard; protein; 260 AA.  
DE Human serine protease protein sequence.  
PN JP11225765-A.  
PD 24-AUG-1999.  
PA (SUNR ) SUNTORY LTD.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 46  
ID AAY41744 standard; protein; 260 AA.  
DE Human PRO322 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 47  
ID AAY03220 standard; protein; 260 AA.  
DE Amino acid sequence of human tumour antigen derived gene-14 protein.  
PN WO9909138-A1.  
PD 25-FEB-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 2; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 48  
ID AAB21322 standard; protein; 260 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 49  
ID AAB44300 standard; protein; 260 AA.  
DE Human PRO322 (UNQ283) protein sequence SEQ ID NO:395.  
PN WO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 50  
ID AAY51131 standard; protein; 260 AA.  
DE Human neuropsin protein.  
PN JP11318461-A.  
PD 24-NOV-1999.  
PA (SHIO/) SHIOZAKA S.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.  
Query Match 45.9%; Score 630.5; DB 3; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 51  
ID AAU12369 standard; protein; 260 AA.  
DE Human PRO322 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 52  
ID AAB53087 standard; protein; 260 AA.  
DE Human angiogenesis-associated protein PRO322, SEQ ID NO:127.  
PN WO200053753-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 53  
ID ABG23373 standard; protein; 260 AA.  
DE Novel human diagnostic protein #23364.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 45.9%; Score 630.5; DB 4; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 54  
ID ABB4852 standard; protein; 260 AA.  
DE Human PRO322 protein sequence SEQ ID NO:72.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 55  
ID AAU81959 standard; protein; 260 AA.  
DE Human PRO322.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 56  
ID ABB95458 standard; protein; 260 AA.  
DE Human angiogenesis related protein PRO322 SEQ ID NO: 72.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 57  
ID ADI17076 standard; protein; 260 AA.  
DE Human NOVX protein homologue SeqID 612.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 5; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 58  
ID ABO17813 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 59  
ID ABO25246 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 60  
ID ABU81067 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 61  
ID ABU72252 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 62  
ID ADA05702 standard; protein; 260 AA.  
DE Human NOV11h protein SEQ ID NO:62.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 63  
ID ABU66767 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 64  
ID ABU84932 standard; protein; 260 AA.  
DE Human secreted and transmembrane PRO polypeptide #8.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 65  
ID ABU59848 standard; protein; 260 AA.  
DE Novel secreted and transmembrane protein PRO322.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 66  
ID ABU61130 standard; protein; 260 AA.  
DE Human PRO322 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 67  
ID ABO25038 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein (PRO) #198.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 6; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 68



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ID ABU80399 standard; protein; 260 AA.
DE Human secreted/transmembrane protein PRO322.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 69
ID ABU67043 standard; protein; 260 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 396.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 70
ID ADA45915 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 71
ID ADA76346 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 72
ID ADA18996 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 73
ID ADA61619 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 74
ID ADB19404 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 75
ID ADB27945 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 76
ID ADA86424 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 77
ID ADB15988 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 78
ID ADA47774 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 79
ID ADA67569 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 80
ID ADB30576 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 81
ID ADA85872 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 82
ID ADA97084 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 83
ID ADA79388 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 84
ID ADA87527 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 85
ID ADB16729 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 45.9%; Score 630.5; DB 6; Length 260;
  Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 86
ID ADA91821 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
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PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 87  
ID ADB14884 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 88  
ID ADA24934 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 89  
ID ADB18845 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 90  
ID ADA94060 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 91  
ID ADB19956 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 92  
ID ADB13268 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 93  
ID ABO43346 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 94  
ID ABO19701 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 95  
ID ADA12595 standard; protein; 260 AA.  
DE Human secreted/transmembrane polypeptide PRO322.  
PN US2003055216-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 96  
ID ADA74522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 97  
ID ADB24755 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 98  
ID ADA82279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 99  
ID ADA75242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 100  
ID ADA85320 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 101  
ID ADA84768 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 102  
ID ADB30024 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 103  
ID ADA80552 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 45.9%; Score 630.5; DB 6; Length 260;  
Query Match 50.2%; Pred. No. 1.1e-40;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 104  
ID ADA75794 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082703-A1.  
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 105
ID ADA47019 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 106
ID ADB25315 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 107
ID ADA93491 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 108
ID ADB26841 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 109
ID ADB31128 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 110
ID ADA61056 standard; protein; 260 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 111
ID ADB24203 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 112
ID ADA96532 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 113
ID ADA81104 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 114
ID ADA95980 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 115
ID ADB26289 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 116
ID ADB21774 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 117
ID ABO19592 standard; protein; 260 AA.
DE Novel human secreted and transmembrane polypeptide #60.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 6; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 118
ID ADA77553 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 119
ID ADB18293 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 120
ID ADA86976 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 121
ID ADA88079 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 122
ID ADA46467 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
```



RESULT 123  
ID ADB28497 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 124  
ID ADB29049 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 125  
ID ADA77001 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 126  
ID ADA88631 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 127  
ID ADA97636 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 128  
ID ADB27393 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 129  
ID ADB22326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 130  
ID ADA67017 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 131  
ID ADB22878 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 132  
ID ADB23651 standard; protein; 260 AA.  
DE Human PRO polypeptide SEQ ID NO 396.

PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 133  
ID ADA92373 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 134  
ID ADB15436 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 135  
ID ADB38688 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 136  
ID ADB38136 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 137  
ID ADB66608 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 138  
ID ADB89688 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 139  
ID ADB90420 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 140  
ID ADB80561 standard; protein; 260 AA.  
DE Ovarian cancer-associated protein #63.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 141  
ID ADB39521 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003082764-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 142
ID ADB73901 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 143
ID ADB47144 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 144
ID ADB86751 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 145
ID ADB76617 standard; protein; 260 AA.
DE Human PRO polypeptide #60.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 146
ID ADB77356 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 147
ID ADB34513 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 148
ID ADB35617 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 149
ID ADB33961 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 45.9%; Score 630.5; DB 7; Length 260;
  RESULT 150
ID ADB35065 standard; protein; 260 AA.
DE Human PRO polypeptide SEQ ID NO 396.
PN US2003077718-A1.
PD 24-APR-2003.

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[illegible]

Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 160  
ID ADC41436 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 161  
ID ADC67491 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 162  
ID ADC62427 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 163  
ID ADC42060 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 164  
ID ADC50437 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 165  
ID ADC71984 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 166  
ID ADC59963 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 167  
ID ADC52970 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 168  
ID ADC57324 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 169  
ID ADC60515 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 170  
ID ADC50990 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 171  
ID ADC65517 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 172  
ID ADC54615 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 173  
ID ADC53576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 174  
ID ADC59099 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 175  
ID ADC55977 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 176  
ID ADC58547 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein Seq ID396.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 177  
ID ADD03221 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;



RESULT 178  
ID ADC90213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 179  
ID ADC69632 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 180  
ID ADC48521 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 181  
ID ADD10050 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 182  
ID ADD04625 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 183  
ID ADC80581 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 184  
ID ADD09100 standard; protein; 260 AA.  
DE Human kallikrein 8 protein SEQ ID NO:2.  
PN WO2003085404-A1.  
PD 16-OCT-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 185  
ID ADD11088 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 186  
ID ADD10361 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 187  
ID ABW00074 standard; protein; 260 AA.

ID ADC47969 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 188  
ID ADC80029 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 189  
ID ADD11321 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 190  
ID ADD09498 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 191  
ID ADD41211 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 192  
ID ADD52350 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 193  
ID ADD53090 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 194  
ID ADD53642 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 195  
ID ADD37114 standard; protein; 260 AA.  
DE Human secreted/transmembrane PRO polypeptide #36.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 196  
ID ABW00074 standard; protein; 260 AA.

DE Human tumour antigen derived gene-14 (TADG-14) protein.  
PN US2002037581-A1.  
PD 28-MAR-2002.  
PA (UABR-) UAB RES FOUND.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 197  
ID ADD51798 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 198  
ID ADD02597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 199  
ID ADD02031 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 200  
ID ADD54213 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 201  
ID ADE49429 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 202  
ID ADD92530 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 203  
ID ADD91426 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 204  
ID ADE04040 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 205  
ID ADE32337 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.

PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 206  
ID ADE22269 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 207  
ID ADD79493 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 208  
ID ADE35483 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 209  
ID ADE16597 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 210  
ID ADD73212 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 211  
ID ADE42029 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 212  
ID ADE17846 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 213  
ID ADD91978 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 214  
ID ADE33441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194767-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 215  
ID ADE333993 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 216  
ID ADD80045 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 217  
ID ADD93082 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 218  
ID ADD72570 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 219  
ID ADE19502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 220  
ID ADE18950 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 221  
ID ADE43146 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 222  
ID ADD95935 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 223  
ID ADE22821 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199064-A1.  
PD 23-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 224  
ID ADD78939 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 225  
ID ADE32889 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 226  
ID ADE42581 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 227  
ID ADE17221 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 228  
ID ADD80597 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 229  
ID ADD89625 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 230  
ID ADE40909 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 231  
ID ADE04708 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 232  
ID ADE92837 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.



Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 233  
ID ADF47235 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 234  
ID ADG21546 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 235  
ID ADG23187 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 236  
ID ADF97522 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 237  
ID ADG80586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 238  
ID ADG52992 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 239  
ID ADG60312 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 240  
ID ADG80034 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 241  
ID ADH55326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 242  
ID ADH55878 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 243  
ID ADI61072 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 244  
ID ADI64097 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 245  
ID ADH81959 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 246  
ID ADH81407 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 247  
ID ADM82576 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 248  
ID ADNI5975 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 249  
ID ADNI6604 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 250  
ID ADN39182 standard; protein; 260 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:500.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.9%; Score 630.5; DB 7; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

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RESULT 251
ID  ADN15423 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003087356-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 7; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 252
ID  ADN14871 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003087357-A1.
PD  08-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 7; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 253
ID  ADI65046 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003207386-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 7; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 254
ID  ADI63545 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003207387-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 7; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 255
ID  ADC81133 standard; protein; 260 AA.
DE  Novel human secreted and transmembrane protein PRO322.
PN  US2003092115-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 256
ID  ADD76581 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003100087-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 257
ID  ADD87945 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003092113-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 258
ID  ADD86349 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003203440-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 259
ID  ADE75797 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003211571-A1.
PD  13-NOV-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 260
ID  ADE89830 standard; protein; 260 AA.
DE  Human secreted/transmembrane protein, PRO322.
PN  05-JUN-2003.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 261
ID  ADE41322 standard; protein; 260 AA.
DE  Human secreted/transmembrane PRO polypeptide #36.
PN  US2003100497-A1.
PD  29-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 262
ID  ADE23373 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003092108-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 263
ID  ADE23925 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003092110-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 264
ID  ADE24568 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003092111-A1.
PD  15-MAY-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 265
ID  ADD87393 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003203439-A1.
PD  30-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 266
ID  ADE89259 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003199062-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 267
ID  ADE18398 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003194794-A1.
PD  16-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 268
ID  ADE88707 standard; protein; 260 AA.
DE  Human PRO polypeptide #198.
PN  US2003199054-A1.
PD  23-OCT-2003.
PA  (GETH ) GENENTECH INC.
    Query Match      45.9%; Score 630.5; DB 8; Length 260;
    Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 269
ID  ADE89830 standard; protein; 260 AA.
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DE Human secreted/transmembrane protein, PRO322.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GROW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 270  
ID ADF61470 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 271  
ID ADF40162 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 272  
ID ADF45958 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 273  
ID ADE94727 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 274  
ID ADE91138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 275

ID ADE95279 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 276  
ID ADE93389 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 277  
ID ADF24354 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 278  
ID ADF40786 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 279  
ID ADF23730 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 280  
ID ADF33713 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 281  
ID ADF34970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 282  
ID ADF27180 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 283  
ID ADF27816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 284  
ID ADE92285 standard; protein; 260 AA.



DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 285  
ID ADE90586 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 286  
ID ADF41410 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 287  
ID ADF33089 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 288  
ID ADF25455 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 289  
ID ADF26556 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 290  
ID ADF34345 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 291  
ID ADF46582 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 292  
ID ADE91733 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 293  
ID ADG02312 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.

PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 294  
ID ADG22098 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 295  
ID ADG20168 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 296  
ID ADF98074 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 297  
ID ADG24291 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 298  
ID ADF98645 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 299  
ID ADG03476 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 300  
ID ADF99197 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 301  
ID ADG16782 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 302  
ID ADG05241 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207375-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 303  
ID ADG19508 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 304  
ID ADG13345 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 305  
ID ADG08402 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 306  
ID ADG15572 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 307  
ID ADF96970 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 308  
ID ADG06155 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 309  
ID ADG23739 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 310  
ID ADG04028 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 311  
ID ADG24929 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207427-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 312  
ID ADG07226 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 313  
ID ADG07778 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 314  
ID ADG55273 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 315  
ID ADG60937 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 316  
ID ADG62041 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 317  
ID ADG82242 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 318  
ID ADG57481 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 319  
ID ADG56929 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 320  
ID ADG55825 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 321  
ID ADG58585 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 322  
ID ADG70951 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 323  
ID ADG58033 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 324  
ID ADG53617 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 325  
ID ADG71503 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 326  
ID ADG50568 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 327  
ID ADG81690 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 328  
ID ADH30652 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 329  
ID ADH12019 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 330  
ID ADG49944 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 331  
ID ADG51816 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 332  
ID ADG52441 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 333  
ID ADG54169 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 334  
ID ADG49320 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 335  
ID ADG81138 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 336  
ID ADG56377 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 337  
ID ADH12643 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 338  
ID ADG48696 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 339



ID ADG61489 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 340  
ID ADH28576 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 341  
ID ADG54721 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 342  
ID ADG59761 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 343  
ID ADG51192 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 344  
ID ADH43505 standard; protein; 260 AA.  
DE Human PRO polypeptide #36.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 345  
ID ADG59136 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 346  
ID ADG62592 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 347  
ID ADI81185 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 348  
ID ADI39730 standard; protein; 260 AA.

DE Human TADG-14 protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 349  
ID ADH25617 standard; protein; 260 AA.  
DE Human neurotrophin homologue related protein sequence SEQ ID NO:395.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 350  
ID ADG09928 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 351  
ID ADI15399 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 352  
ID ADG09276 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 353  
ID ADI14731 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 354  
ID ADI18326 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 355  
ID ADI37154 standard; protein; 260 AA.  
DE Human TADG-14 protein.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 356  
ID ADJ63607 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 357  
ID ADJ77502 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.

PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 358  
ID ADK82850 standard; protein; 260 AA.  
DE Human PRO polypeptide #36.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 359  
ID ADJ65624 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 360  
ID ADM27760 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 361  
ID ADM17394 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 362  
ID ADL07228 standard; protein; 260 AA.  
DE Human secreted/transmembrane protein, PRO322.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 363  
ID ADM42484 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 364  
ID ADN62866 standard; protein; 260 AA.  
DE Human NOV11h.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.

PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 365  
ID ADN04214 standard; protein; 260 AA.  
DE Antipsoriatic protein sequence #302.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 366  
ID ADM28346 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 367  
ID ADI95828 standard; protein; 260 AA.  
DE Human PRO polypeptide #198.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 368  
ID ADI96380 standard; protein; 260 AA.  
DE Novel human secreted and transmembrane protein PRO322.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 369  
ID ADR72883 standard; protein; 260 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 8 (hK8) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 45.9%; Score 630.5; DB 8; Length 260;  
Best Local Similarity 50.2%; Pred. No. 1.1e-40;  
RESULT 370  
ID AAY32853 standard; protein; 305 AA.  
DE Human serine protease protein sequence.  
PN JP11225765-A.  
PD 24-AUG-1999.  
PA (SUNR ) SUNTORY LTD.  
Query Match 45.6%; Score 627; DB 2; Length 305;  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 371  
ID AAB37985 standard; protein; 306 AA.  
DE Human secreted protein encoded by gene 2 clone HWJAE49.  
PN WO200055371-A1.

PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. 45.6%; Score 627; DB 3; Length 306;  
Query Match  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 372  
ID ABP41332 standard; protein; 315 AA.  
DE Human ovarian antigen HCOQP78, SEQ ID NO:2464.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. 45.6%; Score 627; DB 5; Length 315;  
Query Match  
Best Local Similarity 50.9%; Pred. No. 2.4e-40;  
RESULT 373  
ID AAW87703 standard; protein; 260 AA.  
DE A human serine protease designated HGBAB90.  
PN EP887414-A2.  
PD 30-DEC-1998.  
PA (SMIK ) SMITHKLINE BEECHAM PLC. 45.6%; Score 626.5; DB 2; Length 260;  
Query Match  
Best Local Similarity 50.4%; Pred. No. 2.2e-40;  
RESULT 374  
ID AAB21311 standard; protein; 275 AA.  
DE Human neuropsin.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL. 45.6%; Score 626.5; DB 3; Length 275;  
Query Match  
Best Local Similarity 50.4%; Pred. No. 2.3e-40;  
RESULT 375  
ID AAW10694 standard; protein; 260 AA.  
DE Human recombinant neuropsin, used for antibody production.  
PN JP08245700-A.  
PD 24-SEP-1996.  
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK. 45.3%; Score 622.5; DB 2; Length 260;  
Query Match  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 376  
ID AAW12393 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN JP08311099-A.  
PD 26-NOV-1996.  
PA (SHIO/) SHIOZAKA S. 45.3%; Score 622.5; DB 2; Length 260;  
Query Match  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 377  
ID AAY06438 standard; protein; 260 AA.  
DE Human protease HUPM-7.  
PN WO9936550-A2.  
PD 22-JUL-1999.  
PA (INCY-) INCYTE PHARM INC. 45.3%; Score 622.5; DB 2; Length 260;  
Query Match  
Best Local Similarity 49.8%; Pred. No. 4.5e-40;  
RESULT 378  
ID ABB57219 standard; protein; 260 AA.  
DE Mouse ischaemic condition related protein sequence SEQ ID NO:533.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON. 45.3%; Score 622.5; DB 5; Length 260;  
Query Match  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 379  
ID ADI17073 standard; protein; 260 AA.  
DE Murine NOVX protein homologue SeqID 609.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP. 45.3%; Score 622.5; DB 5; Length 260;  
Query Match  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 380  
ID ADI39731 standard; protein; 260 AA.  
DE Mouse neuropsin protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. 45.0%; Score 618.5; DB 5; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 381  
ID ADI37155 standard; protein; 260 AA.  
DE Mouse neuropsin.  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS. 45.3%; Score 622.5; DB 8; Length 260;  
Query Match  
Best Local Similarity 49.0%; Pred. No. 4.5e-40;  
RESULT 382  
ID ADI17074 standard; protein; 260 AA.  
DE Rat NOVX protein homologue SeqID 610.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP. 45.2%; Score 621.5; DB 5; Length 260;  
Query Match  
Best Local Similarity 48.6%; Pred. No. 5.3e-40;  
RESULT 383  
ID AAB21325 standard; protein; 250 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL. 45.0%; Score 618.5; DB 3; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 384  
ID AAY99390 standard; protein; 250 AA.  
DE Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 3; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 385  
ID AAB66139 standard; protein; 250 AA.  
DE Protein of the invention #51.  
PN WO200078961-A1.  
PD 28-DEC-2000.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 4; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 386  
ID AAUI2424 standard; protein; 250 AA.  
DE Human PRO1279 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 4; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 387  
ID ABB50479 standard; protein; 250 AA.  
DE Human secreted protein encoded by gene 179 SEQ ID NO:427.  
PN WO200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. 45.0%; Score 618.5; DB 4; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 388  
ID AAU83684 standard; protein; 250 AA.  
DE Human PRO protein, Seq ID No 186.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 5; Length 250;  
Query Match  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 389  
ID ABG61816 standard; protein; 250 AA.  
DE Prostate cancer-associated protein #17.  
PN WO200230268-A2.  
PD 18-APR-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. 45.0%; Score 618.5; DB 5; Length 250;



Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 390  
ID ABB84920 standard; protein; 250 AA.  
DE Human PRO1279 protein sequence SEQ ID NO:208.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 391  
ID ABB95526 standard; protein; 250 AA.  
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 5; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 392  
ID ABO17868 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 393  
ID ABU80831 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 394  
ID ABO33797 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 395  
ID ABU81122 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 396  
ID ABU56739 standard; protein; 250 AA.  
DE Lung cancer-associated polypeptide #332.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 397  
ID ABU66822 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 398  
ID ABU59903 standard; protein; 250 AA.  
DE Novel secreted and transmembrane protein PRO1279.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 399  
ID ABO25093 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein (PRO) #253.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 400  
ID ABU82140 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 401  
ID ABU67098 standard; protein; 250 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 506.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 402  
ID ADA46025 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 403  
ID ADA76456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 404  
ID ABJ72320 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 405  
ID ADA19106 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 406

ID ADA61729 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 407  
ID ADB19514 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 408  
ID ADB28055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 409  
ID ADA86534 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 410  
ID ADB16098 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 411  
ID ADA47884 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 412  
ID ABO44736 standard; protein; 250 AA.  
DE Novel human secreted protein #179.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 413  
ID ABO33632 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073130-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 414  
ID ADA67679 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 415  
ID ADB30686 standard; protein; 250 AA.

DE Human PRO polypeptide #253.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 416  
ID ADA85982 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 417  
ID ADA97194 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 418  
ID ADA79498 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 419  
ID ADA87637 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 420  
ID ADB16839 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 421  
ID ADA91931 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 422  
ID ADB14994 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 423  
ID ADB18955 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 424  
ID ADA94170 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.

PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 425  
ID ADB20066 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 426  
ID ADB13378 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 427  
ID ABO43401 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 428  
ID ADA74632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 429  
ID ADB24865 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 430  
ID ADA82389 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 431  
ID ADA75352 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 432  
ID ADA85430 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 433  
ID ADA84878 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082708-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 434  
ID ADB30134 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 435  
ID ADA80662 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 436  
ID ADA75904 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 437  
ID ADA47129 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 438  
ID ADB25425 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 439  
ID ADA93601 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 440  
ID ADB26951 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 441  
ID ADB31238 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 442  
ID ABJ72448 standard; protein; 250 AA.  
DE Human PRO1279 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.

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PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 443  
ID ADA61166 standard; protein; 250 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 444  
ID ADB24313 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 445  
ID ADA96642 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 446  
ID ADA81214 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 447  
ID ADA96090 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 448  
ID ADB26399 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 449  
ID ADB21884 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 450  
ID ABO34343 standard; protein; 250 AA.  
DE Human secreted/transmembrane polypeptide PRO 1279.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 6; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 451  
ID ADA77663 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 452  
ID ADB18403 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 453  
ID ADA87086 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 454  
ID ABO44485 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003044841-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 455  
ID ADA88189 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 456  
ID ADA46577 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 457  
ID ADB28607 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 458  
ID ADB29159 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 459  
ID ABO26216 standard; protein; 250 AA.  
DE Human protein from novel secreted protein gene 179.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 460  
ID ADA77111 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;



Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 461  
ID ABO33509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073129-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 462  
ID ADA88741 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 463  
ID ADA97746 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 464  
ID ADB27503 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 465  
ID ADB22436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 466  
ID ABJ72150 standard; protein; 250 AA.  
DE Human membrane bound receptor/protein PRO1279 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 467  
ID ADA67127 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 468  
ID ADB22988 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 469  
ID ADB23761 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 470  
ID ADA92483 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 471  
ID ADB15546 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 472  
ID ADB83676 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 473  
ID ADB80782 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 474  
ID ADB73323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 475  
ID ADB38798 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 476  
ID ADB78405 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 477  
ID ADB38246 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 478  
ID ADB66718 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 479  
ID ADB85053 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.

PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 480  
ID ADB89798 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 481  
ID ADB90530 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 482  
ID ADB80596 standard; protein; 250 AA.  
DE Ovarian cancer-associated protein #81.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 483  
ID ADB39631 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 484  
ID ADB78159 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 485  
ID ADB87225 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 486  
ID ADB84807 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 487  
ID ADB47254 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 488  
ID ADB83922 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003069397-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 489  
ID ADB86861 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 490  
ID ADB73077 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 491  
ID ADB77466 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 492  
ID ADB75388 standard; protein; 250 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 493  
ID ADB34623 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 494  
ID ADB35727 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 495  
ID ADB34071 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 496  
ID ADB35175 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 497  
ID ADB36279 standard; protein; 250 AA.  
DE Human PRO polypeptide SEQ ID NO 506.  
PN US2003077720-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 498  
ID ADB46674 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 499  
ID ADC18039 standard; protein; 250 AA.  
DE Human PRO polypeptide #51.  
PN US2003064925-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 500  
ID ADC36915 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 501  
ID ADC21905 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 502  
ID ADC50547 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 503  
ID ADC72094 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 504  
ID ADC60073 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 505  
ID ADC49936 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 506  
ID ADC49135 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 507  
ID ADC49652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 508  
ID ADC47513 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 509  
ID ADC53080 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 510  
ID ADC57434 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 511  
ID ADC60625 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 512  
ID ADC51100 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 513  
ID ADC65627 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 514  
ID ADC54725 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 515  
ID ADC53686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 516  
ID ADC53686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein Seq ID506.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 516  
 ID ADC59209 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein Seq ID506.  
 PN US2003087359-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 517  
 ID ADC56087 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein Seq ID506.  
 PN US2003087360-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 518  
 ID ADC58657 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein Seq ID506.  
 PN US2003087346-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 519  
 ID ADC47258 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003105288-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 520  
 ID ADD03331 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003092104-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 521  
 ID ADC90323 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003087348-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 522  
 ID ADC69742 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194770-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 523  
 ID ADC48631 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194773-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 524  
 ID ADD10160 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194776-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 525  
 ID ADC78133 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003096972-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 526  
 ID ADD04735 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003087354-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 527  
 ID ADD06368 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003073816-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 528  
 ID ADC80691 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003092103-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 529  
 ID ADD11198 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194774-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 530  
 ID ADD10497 standard; protein; 250 AA.  
 DE Human secreted/transmembrane PRO polypeptide #104.  
 PN US2003105011-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 531  
 ID ADC48079 standard; protein; 250 AA.  
 DE Human PRO polypeptide #253.  
 PN US2003194771-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 532  
 ID ADC77887 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003088066-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 533  
 ID ADC80139 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003087358-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
 RESULT 534  
 ID ADC80139 standard; protein; 250 AA.  
 DE Novel human secreted and transmembrane protein PRO1279.  
 PN US2003087358-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 45.0%; Score 618.5; DB 7; Length 250;  
 Best Local Similarity 48.2%; Pred. No. 8.7e-40;



ID ADD11457 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 535  
ID ADD09608 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 536  
ID ADD50850 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 537  
ID ADD41321 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 538  
ID ADD52460 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 539  
ID ADD51096 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 540  
ID ADD70685 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003099625-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 541  
ID ADD39762 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003083462-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 542  
ID ADD53200 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 543  
ID ADD53752 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 544  
ID ADD70208 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003054406-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 545  
ID ADD37250 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 546  
ID ADD38329 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096955-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 547  
ID ADD39285 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003096954-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 548  
ID ADD51908 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 549  
ID ADD02707 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 550  
ID ADD50577 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 551  
ID ADD02141 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 552  
ID ADD54323 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.

PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 553  
ID ADD50331 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 554  
ID ADD38808 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003092061-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 555  
ID ADD40239 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003082627-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 556  
ID ADD51342 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 557  
ID ADE50460 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 558  
ID ADD92640 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 559  
ID ADD91536 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 560  
ID ADE04150 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 561  
ID ADE20072 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003092883-A1.

PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 562  
ID ADE32447 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 563  
ID ADE22379 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 564  
ID ADD79603 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 565  
ID ADE42139 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 566  
ID ADE17956 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 567  
ID ADD92088 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 568  
ID ADE33551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 569  
ID ADE34103 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 570  
ID ADD80155 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207417-A1.  
PD 06-NOV-2003.

Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 580				
ID ADE32999 standard; protein; 250 AA.				
DE Novel human secreted and transmembrane protein PRO1279.				
PN US2003194766-A1.				
PD 16-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 581				
ID ADE42691 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003199032-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 582				
ID ADD80707 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003207418-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 583				
ID ADD89735 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003199028-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 584				
ID ADE41019 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003199031-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 585				
ID ADE04818 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003199034-A1.				
PD 23-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 586				
ID ADE92947 standard; protein; 250 AA.				
DE Human PRO polypeptide #253.				
PN US2003194777-A1.				
PD 16-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 587				
ID ADF29966 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204053-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 588				
ID ADF55859 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204054-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 589				
ID ADF55859 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204054-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 590				
ID ADF55859 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204054-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 591				
ID ADF55859 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204054-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	45.0%;	Score 618.5;	DB 7;	Length 250;
Best Local Similarity	48.2%;	Pred. No. 8.7e-40;		
RESULT 592				
ID ADF55859 standard; protein; 250 AA.				
DE Human secreted/transmembrane protein PRO1279.				
PN US2003204054-A1.				
PD 30-OCT-2003.				
PA (GETH ) GENENTECH INC.				

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 589  
ID ADG21656 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 590  
ID ADG23297 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 591  
ID ADF97632 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 592  
ID ADG80696 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 593  
ID ADG80144 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 594  
ID ADH55436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 595  
ID ADH5988 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 596  
ID ADH9363 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 597  
ID ADI64207 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 598  
ID ADI65156 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 599  
ID ADH82069 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 600  
ID ADH81517 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 601  
ID ADM82686 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 602  
ID ADN16085 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 603  
ID ADN16714 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 604  
ID ADN39242 standard; protein; 250 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 605  
ID ADN15533 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 606  
ID ADN14981 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 607  
ID ADI65156 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;



ID ADI63655 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 7; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 608  
ID ADC4889 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 609  
ID ADC81243 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 610  
ID ADE21060 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100735-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 611  
ID ADE05904 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100728-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 612  
ID ADD76691 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 613  
ID ADD75133 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100712-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 614  
ID ADD75879 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100717-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 615  
ID ADD85111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100722-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 616  
ID ADD86937 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100738-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 617  
ID ADE20814 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100734-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 618  
ID ADE39111 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096362-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 619  
ID ADD88055 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 620  
ID ADD86459 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 621  
ID ADE05658 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 622  
ID ADD73643 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 623  
ID ADE75907 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 624  
ID ADD78483 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 625  
ID ADE41458 standard; protein; 250 AA.  
DE Human secreted/transmembrane PRO polypeptide #104.

PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 626  
ID ADE23483 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 627  
ID ADE21306 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 628  
ID ADD77421 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 629  
ID ADE20568 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 630  
ID ADD75633 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 631  
ID ADD74149 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 632  
ID ADD74395 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 633  
ID ADD76125 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 634  
ID ADD85617 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100721-A1.

PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 635  
ID ADE24035 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 636  
ID ADE24678 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 637  
ID ADD87503 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 638  
ID ADE05166 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 639  
ID ADD75379 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 640  
ID ADD76923 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 641  
ID ADD86691 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 642  
ID ADE89369 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 643  
ID ADD78159 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003100731-A1.  
PD 29-MAY-2003.



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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 662
ID ADF29489 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 663
ID ADF35080 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 664
ID ADE97020 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 665
ID ADE92395 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 666
ID ADE90696 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 667
ID ADE91843 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 668
ID ADG05699 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 669
ID ADG27253 standard; protein; 250 AA.
DE Human PRO polypeptide #93.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 670
ID ADG02422 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 671
ID ADG22208 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 672
ID ADG20278 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 673
ID ADF98184 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 674
ID ADG24401 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PRO1279.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 675
ID ADF98755 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 676
ID ADG03586 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 677
ID ADF99307 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 678
ID ADG16892 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 679
ID ADG05351 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 680
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ID ADG19618 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 681  
ID ADG11316 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096967-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 682  
ID ADG13455 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 683  
ID ADG08512 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 684  
ID ADG15682 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 685  
ID ADG12095 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 686  
ID ADF97080 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 687  
ID ADG06265 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 688  
ID ADG23849 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 689  
ID ADG04138 standard; protein; 250 AA.

DE Human PRO polypeptide #253.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 690  
ID ADG25039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 691  
ID ADF94652 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 692  
ID ADG07336 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 693  
ID ADG07888 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 694  
ID ADG06748 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 695  
ID ADG55383 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 696  
ID ADG61047 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 697  
ID ADG62151 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 698  
ID ADH03058 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.

PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 699  
ID ADG82352 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 700  
ID ADG57591 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 701  
ID ADG57039 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 702  
ID ADG55935 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 703  
ID ADG58695 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 704  
ID ADG71061 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 705  
ID ADH04012 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 706  
ID ADH03535 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 707  
ID ADH39092 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096965-A1.

PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 708  
ID ADG58143 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 709  
ID ADG53727 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 710  
ID ADG71613 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 711  
ID ADG81800 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 712  
ID ADH30762 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 713  
ID ADH12129 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 714  
ID ADG52551 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 715  
ID ADG54279 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 716  
ID ADG81248 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 717  
ID ADG56487 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 718  
ID ADH12753 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 719  
ID ADG61599 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 720  
ID ADH28686 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 721  
ID ADG54831 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 722  
ID ADG59871 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 723  
ID ADH43641 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 724  
ID ADG34182 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 725  
ID ADH04489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 726  
ID ADI81295 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 727  
ID ADI33652 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 728  
ID ADH69746 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004019183-A1.  
PD 29-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 729  
ID ADH61490 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004014130-A1.  
PD 22-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 730  
ID ADG10038 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 731  
ID ADI15509 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 732  
ID ADG09386 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 733  
ID ADI14841 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 734  
ID ADI29907 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 735  
ID ADH04489 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 250;

RESULT 735  
ID ADI18436 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 736  
ID ADM27304 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 737  
ID ADJ63717 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 738  
ID ADJ77612 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 739  
ID ADK82986 standard; protein; 250 AA.  
DE Human PRO polypeptide #104.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 740  
ID ADK66662 standard; protein; 250 AA.  
DE Human PRO polypeptide #93.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 741  
ID ADJ65734 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 742  
ID ADM27870 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 743  
ID ADM42594 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 744

ID ADL94689 standard; protein; 250 AA.  
DE Human secreted/transmembrane protein PRO1279.  
PN US2004073015-A1.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 745  
ID ADM28456 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 746  
ID ADI95938 standard; protein; 250 AA.  
DE Human PRO polypeptide #253.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 747  
ID ADI96490 standard; protein; 250 AA.  
DE Novel human secreted and transmembrane protein PRO1279.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 748  
ID ADR72632 standard; protein; 250 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 749  
ID ADR72890 standard; protein; 250 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 750  
ID ADS34892 standard; protein; 250 AA.  
DE Human autoimmune disease-related protein - SEQ ID 106.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP. 45.0%; Score 618.5; DB 8; Length 250;  
Query Match 48.2%; Pred. No. 8.7e-40;  
Best Local Similarity 48.2%; Pred. No. 8.7e-40;  
RESULT 751  
ID AAY42439 standard; protein; 282 AA.  
DE CASB12 amino acid sequence.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. 45.0%; Score 618.5; DB 2; Length 282;  
Query Match 48.2%; Pred. No. 9.9e-40;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 752  
ID AAB11712 standard; protein; 282 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.  
PN WO20031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD. 45.0%; Score 618.5; DB 3; Length 282;  
Query Match 48.2%; Pred. No. 9.9e-40;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 753  
ID AAY43636 standard; protein; 282 AA.



DE A human prostate-associated serum protease (PRASP).  
PN WO9941387-A2.  
PD 19-AUG-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 45.0%; Score 618.5; DB 3; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 754  
ID ADN11325 standard; protein; 282 AA.  
DE Human kallikrein-11, marker for prostate cancer.  
PN WO2004029616-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 755  
ID ADQ17587 standard; protein; 282 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 404.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 756  
ID ADR72631 standard; protein; 282 AA.  
DE Human renal cell carcinoma-related kallikrein 11 (hK11) protein 1.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 757  
ID ADR72889 standard; protein; 282 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein1.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 758  
ID ADS34893 standard; protein; 282 AA.  
DE Human autoimmune disease-related protein - SEQ ID 107.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 45.0%; Score 618.5; DB 8; Length 282;  
Best Local Similarity 48.2%; Pred. No. 9.9e-40;  
RESULT 759  
ID AAY42440 standard; protein; 281 AA.  
DE CASB12 polypeptide derived from Expressed Sequence Tag products.  
PN WO9949055-A1.  
PD 30-SEP-1999.  
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 44.6%; Score 612.5; DB 2; Length 281;  
Best Local Similarity 48.0%; Pred. No. 2.8e-39;  
RESULT 760  
ID AAB36482 standard; protein; 288 AA.  
DE Fusion gene with human serine protease catalytic domain protein #13.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.9%; Score 602.5; DB 3; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 761  
ID AAB67542 standard; protein; 288 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH) ORTHO-MCNEIL PHARM INC.  
Query Match 43.9%; Score 602.5; DB 4; Length 288;  
Best Local Similarity 51.1%; Pred. No. 1.7e-38;  
RESULT 762  
ID AAY36093 standard; protein; 250 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 478.

PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST-) GENSET.  
Query Match 43.8%; Score 601.5; DB 2; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 763  
ID ADP19401 standard; protein; 250 AA.  
DE Human secreted polypeptide #252.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST) GENSET SA.  
Query Match 43.8%; Score 601.5; DB 8; Length 250;  
Best Local Similarity 47.4%; Pred. No. 1.8e-38;  
RESULT 764  
ID AAB11714 standard; protein; 275 AA.  
DE Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO) FUSO PHARM IND LTD.  
Query Match 43.7%; Score 601; DB 3; Length 275;  
Best Local Similarity 44.2%; Pred. No. 2.1e-38;  
RESULT 765  
ID AAU82732 standard; protein; 320 AA.  
DE Amino acid sequence of novel human protease #31.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 766  
ID AAE19166 standard; protein; 320 AA.  
DE Human protease, PRIS-3 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 43.6%; Score 599.5; DB 5; Length 320;  
Best Local Similarity 46.4%; Pred. No. 3.3e-38;  
RESULT 767  
ID ADI17075 standard; protein; 225 AA.  
DE Murine NOVX protein homologue SeqID 611.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 43.6%; Score 599; DB 5; Length 225;  
Best Local Similarity 49.8%; Pred. No. 2.5e-38;  
RESULT 768  
ID AAU79390 standard; protein; 256 AA.  
DE Novel human kallikrein KLK15.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 5; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 769  
ID ADN10932 standard; protein; 256 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 43.6%; Score 599; DB 8; Length 256;  
Best Local Similarity 47.1%; Pred. No. 2.8e-38;  
RESULT 770  
ID AAB36483 standard; protein; 289 AA.  
DE Fusion gene with human serine protease catalytic domain protein #14.  
PN WO200066709-A2.  
PD 09-NOV-2000.  
PA (ORTH) ORTHO-MCNEIL PHARM RES INC.  
Query Match 43.6%; Score 598.5; DB 3; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-38;  
RESULT 771  
ID AAB67543 standard; protein; 289 AA.  
DE Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.  
PN WO200116289-A2.

PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 43.6%; Score 598.5; DB 4; Length 289;  
Best Local Similarity 49.1%; Pred. No. 3.5e-38;  
RESULT 772  
ID AAB08017 standard; protein; 248 AA.  
DE Human PS133 consensus protein sequence.  
PN US6232456-B1.  
PD 15-MAY-2001.  
PA (ABBO ) ABBOTT LAB.  
Query Match 43.5%; Score 597.5; DB 4; Length 248;  
Best Local Similarity 47.8%; Pred. No. 3.6e-38;  
RESULT 773  
ID AAB11713 standard; protein; 276 AA.  
DE Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.  
PN WO200031257-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 43.5%; Score 597.5; DB 3; Length 276;  
Best Local Similarity 47.0%; Pred. No. 4e-38;  
RESULT 774  
ID ADC31389 standard; protein; 298 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1471.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 43.3%; Score 595; DB 7; Length 298;  
Best Local Similarity 48.1%; Pred. No. 6.8e-38;  
RESULT 775  
ID ADI17077 standard; protein; 260 AA.  
DE Human NOVX protein homologue SeqID 613.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 43.2%; Score 593.5; DB 5; Length 260;  
Best Local Similarity 48.6%; Pred. No. 7.7e-38;  
RESULT 776  
ID AAB21312 standard; protein; 228 AA.  
DE Human TLSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 43.1%; Score 592; DB 3; Length 228;  
Best Local Similarity 49.3%; Pred. No. 8.7e-38;  
RESULT 777  
ID AAW08475 standard; protein; 247 AA.  
DE Porcine trypsinogen.  
PN WO9700316-A1.  
PD 03-JAN-1997.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 41.7%; Score 573; DB 2; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 778  
ID ABB98258 standard; protein; 247 AA.  
DE Pig trypsinogen SEQ ID NO 1.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 41.7%; Score 573; DB 5; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 779  
ID ADJ92132 standard; protein; 247 AA.  
DE Pig pro-trypsin.  
PN US2004043455-A1.  
PD 04-MAR-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
Query Match 41.7%; Score 573; DB 8; Length 247;  
Best Local Similarity 45.6%; Pred. No. 2.8e-36;  
RESULT 780  
ID AAB21306 standard; protein; 251 AA.  
DE Human KLK-L6 protein #2.  
PN WO200053776-A2.

PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 3; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 781  
ID ADN10930 standard; protein; 251 AA.  
DE Human kallikrein 14, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 569.5; DB 8; Length 251;  
Best Local Similarity 46.9%; Pred. No. 5.2e-36;  
RESULT 782  
ID ABJ26666 standard; protein; 267 AA.  
DE Human protein modification + maintenance molecule protein SEQ ID NO 20.  
PN WO2003000844-A2.  
PD 03-JAN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 41.4%; Score 569.5; DB 6; Length 267;  
Best Local Similarity 46.9%; Pred. No. 5.6e-36;  
RESULT 783  
ID AAB21298 standard; protein; 250 AA.  
DE Human KLK-L3 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 3; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 784  
ID ABP64969 standard; protein; 250 AA.  
DE Human protein SEQ ID 629.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 41.4%; Score 568.5; DB 5; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 785  
ID ABR55400 standard; protein; 250 AA.  
DE Amino acid sequence of human kallikrein 9 (hK9).  
PN WO2003033731-A2.  
PD 24-APR-2003.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.4%; Score 568.5; DB 6; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 786  
ID ADN05516 standard; protein; 250 AA.  
DE Antipsoriatic protein sequence #924.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.4%; Score 568.5; DB 8; Length 250;  
Best Local Similarity 46.7%; Pred. No. 6.2e-36;  
RESULT 787  
ID AAB21300 standard; protein; 277 AA.  
DE Human KLK-L4 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.3%; Score 567; DB 3; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 788  
ID ABO00554 standard; protein; 277 AA.  
DE Novel human polypeptide #141.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 41.3%; Score 567; DB 6; Length 277;  
Best Local Similarity 46.8%; Pred. No. 9e-36;  
RESULT 789  
ID ADL71094 standard; protein; 277 AA.  
DE Human kallikrein 13 protein SEQ ID NO:1.  
PN WO2004021009-A2.  
PD 11-MAR-2004.

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PA (MOUN ) MOUNT SINAI HOSPITAL.
  Query Match      41.3%; Score 567; DB 8; Length 277;
  Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 790
ID ADN04184 standard; protein; 277 AA.
DE Antipsoriatic protein sequence #287.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH ) GENENTECH INC.
  Query Match      41.3%; Score 567; DB 8; Length 277;
  Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 791
ID ADR141575 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID576.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
  Query Match      41.3%; Score 567; DB 8; Length 277;
  Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 792
ID AAU16971 standard; protein; 251 AA.
DE Human novel secreted protein, SEQ ID 212.
PN WO200155441-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      41.2%; Score 566.5; DB 4; Length 251;
  Best Local Similarity 46.9%; Pred. No. 8.9e-36;
RESULT 793
ID AAU23217 standard; protein; 247 AA.
DE Novel human enzyme polypeptide #303.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      41.1%; Score 564.5; DB 4; Length 247;
  Best Local Similarity 46.9%; Pred. No. 1.3e-35;
RESULT 794
ID AAY16777 standard; protein; 293 AA.
DE Human keratinocyte derived protease (KDP).
PN WO9918219-A1.
PD 15-APR-1999.
PA (PROC ) PROCTER & GAMBLE CO.
  Query Match      41.1%; Score 564.5; DB 2; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 795
ID AAY30524 standard; protein; 293 AA.
DE Human PDSP-1 protein.
PN WO9946391-A2.
PD 16-SEP-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
  Query Match      41.1%; Score 564.5; DB 2; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 796
ID AAY38412 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      41.1%; Score 564.5; DB 2; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 797
ID AAY38426 standard; protein; 293 AA.
DE Human secreted protein encoded by gene No. 27.
PN WO9935158-A1.
PD 15-JUL-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      41.1%; Score 564.5; DB 2; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 798
ID AAY66726 standard; protein; 293 AA.
DE Membrane-bound protein PRO1132.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 3; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 799
ID AAB21296 standard; protein; 293 AA.
DE Human KLK-L2 protein.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL.
  Query Match      41.1%; Score 564.5; DB 3; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 800
ID AAU12399 standard; protein; 293 AA.
DE Human PRO1132 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 4; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 801
ID AAB65249 standard; protein; 293 AA.
DE Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 4; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 802
ID AAU81966 standard; protein; 293 AA.
DE Human PRO1132.
PN WO200109327-A2.
PD 08-FEB-2001.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 5; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 803
ID ABUS8064 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003027163-A1.
PD 06-FEB-2003.
  Query Match      41.1%; Score 564.5; DB 6; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 804
ID ABUS9142 standard; protein; 293 AA.
DE Novel human secreted or transmembrane protein PRO1132.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 6; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 805
ID ABUS2654 standard; protein; 293 AA.
DE Human secreted/transmembrane protein PRO1132.
PN US2003032023-A1.
PD 13-FEB-2003.
  Query Match      41.1%; Score 564.5; DB 6; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 806
ID ABO17843 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match      41.1%; Score 564.5; DB 6; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 807
ID ADA57425 standard; protein; 293 AA.
DE Human secreted protein #257.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
  Query Match      41.1%; Score 564.5; DB 6; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 808
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ID ADA56974 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 809  
ID ADA57427 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 810  
ID ADA57428 standard; protein; 293 AA.  
DE Human secreted protein #257.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 811  
ID ABU60573 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 812  
ID ABU13955 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 813  
ID ABU81097 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 814  
ID ABU72540 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 815  
ID ABU66797 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 816  
ID ADA41303 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 817  
ID ADA41305 standard; protein; 293 AA.

DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 818  
ID ADA40825 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 819  
ID ADA41306 standard; protein; 293 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 820  
ID ABU59878 standard; protein; 293 AA.  
DE Novel secreted and transmembrane protein PRO1132.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 821  
ID ABU59289 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 822  
ID ABO25986 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 823  
ID ABO25068 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein (PRO) #228.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 824  
ID ABU58995 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, #130.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 825  
ID ABU92373 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 826  
ID ABU59438 standard; protein; 293 AA.  
DE Novel human secreted or transmembrane protein PRO1346.  
PN US2003027985-A1.  
PD 06-FEB-2003.



Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 827  
ID ABU67073 standard; protein; 293 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 456.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 828  
ID ABU92204 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 829  
ID ABU10910 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 830  
ID ABU81662 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 831  
ID ABU88601 standard; protein; 293 AA.  
DE Human secreted and transmembrane polypeptide PRO1132.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 832  
ID ABO34115 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 833  
ID ADA45975 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 834  
ID ADA76406 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 835  
ID ADA19056 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 836

ID ADA61679 standard; protein; 293 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 837  
ID ADB19464 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 838  
ID ADB28005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 839  
ID ADA86484 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 840  
ID ADB16048 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 841  
ID ADA37820 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 842  
ID ADA47834 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 843  
ID ADA21506 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 844  
ID ADA10293 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein, PRO1132.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 845  
ID ADA67629 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068795-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 846  
ID ADB30636 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 847  
ID ADA85932 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 848  
ID ADA17837 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 849  
ID ADA97144 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 850  
ID ADA79448 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 851  
ID ADA87587 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 852  
ID ADB16789 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 853  
ID ADA27945 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 854  
ID ADA91881 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 855  
ID ADB14944 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 856  
ID ADB18905 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 857  
ID ADA94120 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 858  
ID ADB20016 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 859  
ID ADB13328 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 860  
ID ABO43376 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 861  
ID ADA94525 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 862  
ID ADA74582 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 863  
ID ADB24815 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 864

ID ADA82339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 865  
ID ADA75302 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 866  
ID ADA85380 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 867  
ID ADA84828 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 868  
ID ADB30084 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 869  
ID ADA80612 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 870  
ID ADA75854 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 871  
ID ADA38750 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 872  
ID ADA47079 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 873  
ID ADB25375 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.

PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 874  
ID ADA93551 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 875  
ID ADB26901 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 876  
ID ADB31188 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 877  
ID ADA92871 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 878  
ID ADA61116 standard; protein; 293 AA.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 879  
ID ADB24263 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 880  
ID ADA96592 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 881  
ID ADA81164 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 882  
ID ADA96040 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082759-A1.  
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 883  
ID ADB26349 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 884  
ID ADB21834 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 6; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 885  
ID ADA77613 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 886  
ID ADB18353 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 887  
ID ADA87036 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 888  
ID ADA88139 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 889  
ID ADA46527 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 890  
ID ADB28557 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 891  
ID ADB29109 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 892  
ID ABO53201 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 893  
ID ADA77061 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 894  
ID ADA22432 standard; protein; 293 AA.  
DE Human secreted/transmembrane polypeptide PRO1132.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 895  
ID ADA88691 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 896  
ID ADA97696 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 897  
ID ADB27453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 898  
ID ADB22386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 899  
ID ABO22571 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 900  
ID ADA06598 standard; protein; 293 AA.  
DE Human secreted/transmembrane PRO polypeptide #96.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 901  
ID ADA39291 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003059782-A1.  
PD 27-MAR-2003.



Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 902  
ID ADA67077 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 903  
ID ADB22938 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 904  
ID ADB23711 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 905  
ID ADA92433 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 906  
ID ADB15496 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 907  
ID ADB38748 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 908  
ID ADB96317 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 909  
ID ADB38196 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 910  
ID ADB66668 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 911  
ID ADB89748 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 912  
ID ADB90480 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 913  
ID ADB80490 standard; protein; 293 AA.  
DE Ovarian cancer-associated protein #27.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 914  
ID ADB39581 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 915  
ID ADB47204 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 916  
ID ADB86811 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 917  
ID ADB77416 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 918  
ID ADB34573 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 919  
ID ADB35677 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 920  
ID ADB35677 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

ID ADB34021 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 921  
ID ADB35125 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 922  
ID ADB36229 standard; protein; 293 AA.  
DE Human PRO polypeptide SEQ ID NO 456.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 923  
ID ADB46624 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 924  
ID ADC57789 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 925  
ID ADC55153 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 926  
ID ADC12020 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 927  
ID ADC56442 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 928  
ID ADC07497 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 929  
ID ADC11487 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 930  
ID ADC50497 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 931  
ID ADC72044 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 932  
ID ADC60023 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 933  
ID ADC53030 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 934  
ID ADC57384 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 935  
ID ADC60575 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 936  
ID ADC51050 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 937  
ID ADC65577 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 938  
ID ADC54675 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 939

ID ADC53636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 940  
ID ADC59159 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 941  
ID ADC56037 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 942  
ID ADC58607 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein Seq ID456.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 943  
ID ADC14609 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 944  
ID ADD08141 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 945  
ID ADD03281 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 946  
ID ADC90273 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 947  
ID ADC81966 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 948  
ID ADC69692 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194770-A1.  
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 949  
ID ADC48581 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 950  
ID ADD10110 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 951  
ID ADD07608 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 952  
ID ADD04685 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 953  
ID ADC82499 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 954  
ID ADC80641 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 955  
ID ADD11148 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 956  
ID ADC48029 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 957  
ID ADD08679 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

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RESULT 958
ID ADC80089 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 959
ID ADD06928 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 960
ID ADD09558 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 961
ID ADC83175 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 962
ID ADD41271 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 963
ID ADD52410 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 964
ID ADD53150 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 965
ID ADD53702 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 966
ID ADD55282 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 967
ID ADD56240 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 968
ID ADD51858 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 969
ID ADD02657 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 970
ID ADD02091 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 971
ID ADD54273 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 972
ID ADD54678 standard; protein; 293 AA.
DE Human PRO polypeptide #96.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 973
ID ADD92590 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 974
ID ADD91486 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 975
ID ADE04100 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 976
ID ADE26832 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 986			
ID	ADD931142' standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003194768-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 987			
ID	ADE19562 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003199025-A1.		
PD	23-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 988			
ID	ADE19010 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003199026-A1.		
PD	23-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 989			
ID	AD43206 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003199033-A1.		
PD	23-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 990			
ID	ADD95995 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003199059-A1.		
PD	23-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 991			
ID	ADE22881 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003199064-A1.		
PD	23-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 992			
ID	ADD78999 standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003203429-A1.		
PD	30-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 993			
ID	ADE26299 standard; protein; 293 AA.		
DE	Novel human secreted and transmembrane protein PRO1132.		
PN	US2003087305-A1.		
PD	08-MAY-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 994			
ID	ADE32949 standard; protein; 293 AA.		
DE	Novel human secreted and transmembrane protein PRO1132.		
PN	US2003194766-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			
RESULT 995			
ID	ADD931142' standard; protein; 293 AA.		
DE	Human PRO polypeptide #228.		
PN	US2003194768-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match		41.1%;	Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;			

ID ADE42641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 996  
ID ADD80657 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 997  
ID ADD89685 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 998  
ID ADE04768 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 999  
ID ADE04768 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1000  
ID ADE92897 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1001  
ID ADF67236 standard; protein; 293 AA.  
DE Human PRO1132 amino acid sequence SEQ ID NO:309.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1002  
ID ADG21606 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1003  
ID ADG23247 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1004  
ID ADF97582 standard; protein; 293 AA.

DE Human PRO polypeptide #228.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1005  
ID ADG80646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1006  
ID ADG80094 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1007  
ID ADH55386 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1008  
ID ADH55938 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1009  
ID ADI35490 standard; protein; 293 AA.  
DE Human PRO polypeptide #96.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1010  
ID ADI64157 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1011  
ID ADI65106 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1012  
ID ADI63605 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1013  
ID ADH82019 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207388-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1014  
ID ADH9982 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1015  
ID ADH81467 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1016  
ID ADM82636 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1017  
ID ADN16035 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1018  
ID ADN16664 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1019  
ID ADN39198 standard; protein; 293 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:516.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1020  
ID ADN15483 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1021  
ID ADN14931 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 7; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1022  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1023  
ID ADD76641 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1024  
ID ADD88005 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1025  
ID ADD86409 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1026  
ID ADE75857 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1027  
ID ADE23433 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1028  
ID ADE23985 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1029  
ID ADE24628 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1030  
ID ADD87453 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1031  
ID ADE89319 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1032  
ID ADC81193 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1032  
ID ADE18458 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1033  
ID ADE88767 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1034  
ID ADE94787 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1035  
ID ADE91198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1036  
ID ADF35435 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1037  
ID ADE95339 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1038  
ID ADE93449 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1039  
ID ADF35030 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1040  
ID ADE92345 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1041

ID ADE90646 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1042  
ID ADE91793 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1043  
ID ADG11685 standard; protein; 293 AA.  
DE Human PRO1132 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1044  
ID ADG02372 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1045  
ID ADG22158 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1046  
ID ADG20228 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1047  
ID ADF98134 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1048  
ID ADG24351 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1049  
ID ADF98705 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1050  
ID ADG03536 standard; protein; 293 AA.



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DE Human PRO polypeptide #228.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1051
ID ADF99257 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1052
ID ADG16842 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1053
ID ADG05301 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1054
ID ADG19568 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1055
ID ADG13405 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1056
ID ADG08462 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1057
ID ADG15632 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1058
ID ADF97030 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1059
ID ADG06215 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1060
ID ADG23799 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1061
ID ADG04088 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1062
ID ADG24989 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1063
ID ADG07286 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1064
ID ADG07838 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1065
ID ADG55333 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1066
ID ADG60997 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1067
ID ADG62101 standard; protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 41.1%; Score 564.5; DB 8; Length 293;
  Best Local Similarity 45.3%; Pred. No. 1.5e-35;
  RESULT 1068
ID ADG82302 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207358-A1.
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PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1069  
ID ADG57541 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1070  
ID ADG56989 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1071  
ID ADG55885 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1072  
ID ADG58645 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1073  
ID ADG71011 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1074  
ID ADG58093 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1075  
ID ADG53677 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1076  
ID ADG71563 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1077  
ID ADG81750 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003207805-A1.  
PD 06-NOV-2003.

Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1078  
ID ADH19555 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1079  
ID ADH30712 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1080  
ID ADH12079 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1081  
ID ADG52501 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1082  
ID ADG54229 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1083  
ID ADG81198 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1084  
ID ADG56437 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1085  
ID ADH12703 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1086  
ID ADH21048 standard; protein; 293 AA.  
DE Human secreted/transmembrane protein PRO1132.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;

ID	AD114791 standard; protein; 293 AA.	
DE	Novel human secreted and transmembrane protein PRO1132.	
PN	US2003207383-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1097		
ID	AD118386 standard; protein; 293 AA.	
DE	Novel human secreted and transmembrane protein PRO1132.	
PN	US2003207349-A1.	
PD	06-NOV-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1098		
ID	ADJ63667 standard; protein; 293 AA.	
DE	Novel human secreted and transmembrane protein PRO1132.	
PN	US2004039164-A1.	
PD	26-FEB-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1099		
ID	ADJ77562 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004038336-A1.	
PD	26-FEB-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1100		
ID	ADJ65684 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004038335-A1.	
PD	26-FEB-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1101		
ID	ADM27820 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004048333-A1.	
PD	11-MAR-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1102		
ID	ADK52481 standard; protein; 293 AA.	
DE	Human kallikrein 5 protein.	
PN	WO2004021008-A2.	
PD	11-MAR-2004.	
PA	(MOUN ) MOUNT SINAI HOSPITAL.	
PA	(YOUS/) YOUSEF G.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1103		
ID	ADM42544 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004058424-A1.	
PD	25-MAR-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1104		
ID	ADM28406 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004077064-A1.	
PD	22-APR-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1105		
ID	ADM28406 standard; protein; 293 AA.	
DE	Human PRO polypeptide #228.	
PN	US2004077064-A1.	
PD	22-APR-2004.	
PA	(GETH ) GENENTECH INC.	
Query Match	41.1%; Score 564.5; DB 8; Length 293;	
Best Local Similarity	45.3%; Pred. No. 1.5e-35;	
RESULT 1105		

ID ADI95888 standard; protein; 293 AA.  
DE Human PRO polypeptide #228.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1106  
ID ADI96440 standard; protein; 293 AA.  
DE Novel human secreted and transmembrane protein PRO1132.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1107  
ID ADR72621 standard; protein; 293 AA.  
DE Human renal cell carcinoma-related kallikrein 5 (hK5) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1108  
ID ADR72873 standard; protein; 293 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.1%; Score 564.5; DB 8; Length 293;  
Best Local Similarity 45.3%; Pred. No. 1.5e-35;  
RESULT 1109  
ID AAY14072 standard; protein; 322 AA.  
DE Human BS247 specific epitope.  
PN WO9922027-A1.  
PD 06-MAY-1999.  
PA (ABBO ) ABBOTT LAB.  
Query Match 41.1%; Score 564.5; DB 2; Length 322;  
Best Local Similarity 45.3%; Pred. No. 1.6e-35;  
RESULT 1110  
ID AAW07620 standard; protein; 276 AA.  
DE Human NES1 polypeptide.  
PN WO9639175-A1.  
PD 12-DEC-1996.  
PA (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.  
Query Match 41.0%; Score 564; DB 2; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1111  
ID AAB21327 standard; protein; 276 AA.  
DE Human NES1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 3; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1112  
ID ABG96356 standard; protein; 276 AA.  
DE Human ovarian cancer marker OV32.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 5; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1113  
ID AAU82729 standard; protein; 276 AA.  
DE Amino acid sequence of novel human protease #28.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 41.0%; Score 564; DB 5; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1114  
ID ADB80527 standard; protein; 276 AA.

DE Ovarian cancer-associated protein #46.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1115  
ID ADE40473 standard; protein; 276 AA.  
DE Human kallikrein 10 (gene ID 2045) protein.  
PN WO2003070883-A2.  
PD 28-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1116  
ID ADN39880 standard; protein; 276 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 41.0%; Score 564; DB 7; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1117  
ID ADN04446 standard; protein; 276 AA.  
DE Antipsoriatic protein sequence #416.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1118  
ID ADQ89070 standard; protein; 276 AA.  
DE Human urological disorder related protein 2045 SEQ:22.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1119  
ID ADR72628 standard; protein; 276 AA.  
DE Human renal cell carcinoma-related kallikrein 10 (hK10) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1120  
ID ADR72886 standard; protein; 276 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 10 (hK10) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1121  
ID AAB21305 standard; protein; 237 AA.  
DE Human KLK-L6 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 41.0%; Score 564; DB 8; Length 276;  
Best Local Similarity 45.9%; Pred. No. 1.5e-35;  
RESULT 1122  
ID AAB21299 standard; protein; 256 AA.  
DE Human KLK-L4 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 562; DB 3; Length 237;  
Best Local Similarity 48.1%; Pred. No. 1.9e-35;  
RESULT 1123  
ID AAB21309 standard; protein; 287 AA.  
DE Human KLK-L2.



PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.9%; Score 561.5; DB 3; Length 287;  
Best Local Similarity 46.1%; Pred. No. 2.5e-35;  
RESULT 1124  
ID ABB98259 standard; protein; 228 AA.  
DE Synthetic shortened trypsinogen SEQ ID NO 23.  
PN WO200261064-A2.  
PD 08-AUG-2002.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
Query Match 40.8%; Score 561; DB 5; Length 228;  
Best Local Similarity 46.7%; Pred. No. 2.1e-35;  
RESULT 1125  
ID AAB21310 standard; protein; 239 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 239;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1126  
ID AAR44532 standard; protein; 244 AA.  
DE Zyme APP-cleaving protease.  
PN EP576152-A1.  
PD 29-DEC-1993.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1127  
ID AAW22985 standard; protein; 244 AA.  
DE Human serine protease 59 (SP59).  
PN JP09149790-A.  
PD 10-JUN-1997.  
PA (SUNR ) SUNTORY LTD.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1128  
ID AAW51006 standard; protein; 244 AA.  
DE Protease M, a novel serine protease.  
PN WO9811238-A2.  
PD 19-MAR-1998.  
PA (DAND-) DANA FARBER CANCER INST INC.  
Query Match 40.8%; Score 561; DB 2; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1129  
ID AAB21323 standard; protein; 244 AA.  
DE Human zyme.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 3; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1130  
ID AAE37572 standard; protein; 244 AA.  
DE Human 2047 protein.  
PN WO2003037258-A2.  
PD 08-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 6; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1131  
ID ADB0567 standard; protein; 244 AA.  
DE Ovarian cancer-associated protein #66.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1132  
ID ADN39212 standard; protein; 244 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.

PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.8%; Score 561; DB 7; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1133  
ID ADN04074 standard; protein; 244 AA.  
DE Antipsoriatic protein sequence #232.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1134  
ID ADN29289 standard; protein; 244 AA.  
DE Human kallikrein 6 associated protein.  
PN US2004097452-A1.  
PD 20-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1135  
ID ADQ89076 standard; protein; 244 AA.  
DE Human urological disorder related protein 2047 SEQ:28.  
PN WO2004065576-A2.  
PD 05-AUG-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1136  
ID ADR72624 standard; protein; 244 AA.  
DE Human renal cell carcinoma-related kallikrein 6 (hk6) protein.  
PN WO2004077060-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1137  
ID ADR72876 standard; protein; 244 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 6 (hk6) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.8%; Score 561; DB 8; Length 244;  
Best Local Similarity 46.7%; Pred. No. 2.3e-35;  
RESULT 1138  
ID ABG96357 standard; protein; 244 AA.  
DE Human ovarian cancer marker OV33.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 40.8%; Score 560; DB 5; Length 244;  
Best Local Similarity 46.9%; Pred. No. 2.7e-35;  
RESULT 1139  
ID AAB21297 standard; protein; 296 AA.  
DE Human KLK-L3 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.5%; Score 557; DB 3; Length 296;  
Best Local Similarity 46.1%; Pred. No. 5.7e-35;  
RESULT 1140  
ID AAR67888 standard; protein; 253 AA.  
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).  
PN WO9500651-A1.  
PD 05-JAN-1995.  
PA (SYMB-) SYMBICOM AB.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1141  
ID AAW05383 standard; protein; 253 AA.  
DE Human amyloid precursor protein protease.  
PN WO9631122-A1.

PD 10-OCT-1996.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 40.4%; Score 555; DB 2; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1142  
ID ABB84421 standard; peptide; 253 AA.  
DE Human SCCE protein N-terminal fragment SEQ ID 48.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1143  
ID ABB84406 standard; protein; 253 AA.  
DE Human SCCE protein.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1144  
ID AAU82740 standard; protein; 253 AA.  
DE Amino acid sequence of novel human protease #39.  
PN WO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 40.4%; Score 555; DB 5; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1145  
ID ABU07440 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #43.  
PN WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1146  
ID ABU07471 standard; protein; 253 AA.  
DE Protein differentially regulated in prostate cancer #74.  
PN WO200281638-A2.  
PD 17-OCT-2002.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1147  
ID ABR58471 standard; protein; 253 AA.  
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.  
PN WO2003029468-A1.  
PD 10-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 40.4%; Score 555; DB 6; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1148  
ID ADB80484 standard; protein; 253 AA.  
DE Ovarian cancer-associated protein #24.  
PN WO2002102235-A2.  
PD 27-DEC-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1149  
ID ADJ68833 standard; protein; 253 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID639.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1150  
ID ADN39180 standard; protein; 253 AA.

DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 40.4%; Score 555; DB 7; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1151  
ID ADL06515 standard; protein; 253 AA.  
DE Human tumour-associated antigenic target (TAT) polypeptide #14.  
PN WO2004016225-A2.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1152  
ID ADN04182 standard; protein; 253 AA.  
DE Antipsoriatic protein sequence #286.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1153  
ID ADR72880 standard; protein; 253 AA.  
DE Human ovarian cancer-related tumour marker kallikrein 7 (hK7) protein.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 40.4%; Score 555; DB 8; Length 253;  
Best Local Similarity 44.6%; Pred. No. 6.9e-35;  
RESULT 1154  
ID ADA05734 standard; protein; 252 AA.  
DE Human NOV18b protein SEQ ID NO:94.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.3%; Score 553.5; DB 6; Length 252;  
Best Local Similarity 46.6%; Pred. No. 9e-35;  
RESULT 1155  
ID ADN62898 standard; protein; 252 AA.  
DE Human NOV18b.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPO V A.

PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 40.3%; Score 553.5; DB 8; Length 252;  
Best Local Similarity 46.6%; Pred. No. 9e-35;  
RESULT 1156  
ID AAY08025 standard; protein; 253 AA.  
DE Mouse protease-related protein (PVP).  
PN DE19736198-C1.  
PD 24-DEC-1998.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
Query Match 40.3%; Score 553.5; DB 2; Length 253;  
Best Local Similarity 43.5%; Pred. No. 9e-35;  
RESULT 1157  
ID ADN62896 standard; protein; 250 AA.  
DE Human NOV18a.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWV/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 40.2%; Score 553; DB 8; Length 250;  
Best Local Similarity 44.8%; Pred. No. 9.8e-35;  
RESULT 1158  
ID AAY77494 standard; protein; 229 AA.  
DE Bovine trypsinogen.  
PN WO200005384-A1.  
PD 03-FEB-2000.  
PA (PROD-) PRODIGENE INC.  
Query Match 40.2%; Score 552; DB 3; Length 229;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1159  
ID AAR53638 standard; protein; 230 AA.  
DE Bovine trypsinogen.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (BLIL) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 2; Length 230;  
Best Local Similarity 47.5%; Pred. No. 1.1e-34;  
RESULT 1160  
ID AAY91926 standard; protein; 231 AA.

DE Recombinant trypsin.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 3; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1161  
ID AAB80953 standard; protein; 231 AA.  
DE Bovine met-phe-trypsinogen.  
PN WO200119970-A2.  
PD 22-MAR-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 40.2%; Score 552; DB 4; Length 231;  
Best Local Similarity 46.3%; Pred. No. 1.1e-34;  
RESULT 1162  
ID ADA05732 standard; protein; 250 AA.  
DE Human NOV18a protein SEQ ID NO:92.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 40.2%; Score 552; DB 6; Length 250;  
Best Local Similarity 44.8%; Pred. No. 1.2e-34;  
RESULT 1163  
ID ABB84420 standard; peptide; 249 AA.  
DE Porcine SCCE protein N-terminal fragment SEQ ID 47.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 40.1%; Score 550.5; DB 5; Length 249;  
Best Local Similarity 46.7%; Pred. No. 1.5e-34;  
RESULT 1164  
ID AAB35701 standard; protein; 247 AA.  
DE Human trypsin hL amino acid sequence.  
PN JF2000253887-A.  
PD 19-SEP-2000.  
PA (TTPH-) TT PHARMA KK.  
Query Match 40.0%; Score 549.5; DB 3; Length 247;  
Best Local Similarity 44.0%; Pred. No. 1.8e-34;  
RESULT 1165  
ID AAU86677 standard; protein; 247 AA.  
DE Novel human connective tissue related polypeptide #243.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1166  
ID AAU23752 standard; protein; 247 AA.  
DE Novel human enzyme polypeptide #838.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1167  
ID AAU17043 standard; protein; 247 AA.  
DE Human novel secreted protein, SEQ ID 284.  
PN WO200155441-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 4; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1168  
ID ADB60011 standard; protein; 247 AA.  
DE Connective tissue antigen (CTA) #243.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 39.8%; Score 547.5; DB 7; Length 247;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1169  
ID AAW81767 standard; peptide; 223 AA.

DE Bovine TRYP peptide fragment.  
PN JP10287696-A.  
PD 27-OCT-1998.  
PA (IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.  
Query Match 39.8%; Score 547; DB 2; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1170  
ID AAY69973 standard; protein; 223 AA.  
DE TRYP protein.  
PN WO9962004-A1.  
PD 02-DEC-1999.  
PA (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.  
Query Match 39.8%; Score 547; DB 3; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1171  
ID ABG31841 standard; protein; 223 AA.  
DE Example protein #3 used in three-dimensional structure analysis method.  
PN WO200257954-A1.  
PD 25-JUL-2002.  
PA (MITU) MITSUBISHI CHEM CORP.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 5; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1172  
ID ADC73287 standard; protein; 223 AA.  
DE Bovine 2PTC E protein - SEQ ID 13.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1173  
ID ADD35545 standard; protein; 223 AA.  
DE Cationic bovine trypsinogen TRY1.  
PN WO2003040093-A2.  
PD 15-MAY-2003.  
PA (FARB) BAYER AG.  
Query Match 39.8%; Score 547; DB 7; Length 223;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1174  
ID AAR53637 standard; protein; 224 AA.  
DE Bovine trypsin.  
PN EP597681-A1.  
PD 18-MAY-1994.  
PA (ELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 2; Length 224;  
Best Local Similarity 46.1%; Pred. No. 2.5e-34;  
RESULT 1175  
ID AAY91925 standard; protein; 233 AA.  
DE Trypsinogen analogue.  
PN WO200017332-A1.  
PD 30-MAR-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 39.8%; Score 547; DB 3; Length 233;  
Best Local Similarity 46.1%; Pred. No. 2.6e-34;  
RESULT 1176  
ID ADI39734 standard; protein; 244 AA.  
DE Human protease M (prom) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1177  
ID ADI37158 standard; protein; 244 AA.  
DE Human protease m (Promt).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 39.7%; Score 546; DB 8; Length 244;  
Best Local Similarity 45.8%; Pred. No. 3.3e-34;  
RESULT 1178

ID AAY78974 standard; protein; 247 AA.  
DE Canine cationic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJI YAKUHHN KOGYO KK.  
Query Match 39.7%; Score 546; DB 3; Length 247;  
Best Local Similarity 45.6%; Pred. No. 3.3e-34;  
RESULT 1179  
ID ADA05742 standard; protein; 247 AA.  
DE Human NOV18f protein SEQ ID NO:102.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.7%; Score 546; DB 6; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1180  
ID ADN62906 standard; protein; 247 AA.  
DE Human NOV18f.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 39.7%; Score 546; DB 8; Length 247;  
Best Local Similarity 45.5%; Pred. No. 3.3e-34;  
RESULT 1181  
ID AAB98502 standard; protein; 225 AA.  
DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 39.7%; Score 545; DB 4; Length 225;  
Best Local Similarity 46.5%; Pred. No. 3.6e-34;  
RESULT 1182  
ID AAY78975 standard; protein; 246 AA.  
DE Canine anionic trypsinogen amino acid sequence.  
PN WO200009739-A1.  
PD 24-FEB-2000.  
PA (FUJY) FUJI YAKUHHN KOGYO KK.  
Query Match 39.7%; Score 545; DB 3; Length 246;  
Best Local Similarity 44.2%; Pred. No. 4e-34;  
RESULT 1183



ID AAB21326 standard; protein; 257 AA.  
DE Human HSCCE.  
PN WO2000053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 39.6%; Score 544; DB 3; Length 257;  
Best Local Similarity 44.1%; Pred. No. 5e-34;  
RESULT 1184  
ID AAW64260 standard; protein; 246 AA.  
DE Human amyloid beta-protein precursor inhibitor.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 39.5%; Score 543; DB 2; Length 246;  
Best Local Similarity 44.5%; Pred. No. 5.7e-34;  
RESULT 1185  
ID ADC73299 standard; protein; 220 AA.  
DE Stereostucture-related 2PTC\_E protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 220;  
Best Local Similarity 46.8%; Pred. No. 7.2e-34;  
RESULT 1186  
ID ADC73301 standard; protein; 279 AA.  
DE Stereostucture-related 2PTC protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN ) AJINOMOTO CO INC.  
PA (UMEY/) UMEYAMA H.  
Query Match 39.4%; Score 541; DB 7; Length 279;  
Best Local Similarity 46.8%; Pred. No. 9.2e-34;  
RESULT 1187  
ID ADI16686 standard; protein; 259 AA.  
DE Human NOVX protein to treat human pathological conditions SeqID222.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 39.3%; Score 539.5; DB 5; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1188  
ID ADN42340 standard; protein; 259 AA.  
DE Human novel proteinNOV 62.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V T.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R A.  
PA (LILL/) LI L.  
PA (GANG/) GANGOLLI E A.  
PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D W.  
PA (RAST/) RASTELLI L.  
PA (MILL/) MILLER C E.  
PA (GERL/) GERLACH V.  
PA (TAUP/) TAUPIER R J.  
PA (GUSE/) GUSEV V Y.  
PA (COLM/) COLMAN S D.  
PA (WOLE/) WOLENC A R.  
PA (PENA/) PENNA C E A.  
PA (FURT/) FURTAK K.  
PA (GROS/) GROSSE W M.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
Query Match 39.3%; Score 539.5; DB 8; Length 259;  
Best Local Similarity 44.4%; Pred. No. 1.1e-33;  
RESULT 1189  
ID ABB78122 standard; peptide; 223 AA.

DE Amino acid sequence of trypsin.  
PN US2002072863-A1.  
PD 13-JUN-2002.  
PA (FUIT ) FUJITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1190  
ID ABB83322 standard; protein; 223 AA.  
DE Partial trypsin sequence.  
PN US2002035434-A1.  
PD 21-MAR-2002.  
PA (FUIT ) FUJITSU LTD.  
Query Match 39.2%; Score 538; DB 5; Length 223;  
Best Local Similarity 45.6%; Pred. No. 1.2e-33;  
RESULT 1191  
ID ABB84419 standard; peptide; 243 AA.  
DE Bovine SCCE protein N-terminal fragment SEQ ID 46.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.7%; Score 531.5; DB 5; Length 243;  
Best Local Similarity 43.8%; Pred. No. 4.3e-33;  
RESULT 1192  
ID ABB04644 standard; protein; 240 AA.  
DE Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISB ) JAPAN TOBACCO INC.  
Query Match 38.2%; Score 525; DB 5; Length 240;  
Best Local Similarity 45.7%; Pred. No. 1.3e-32;  
RESULT 1193  
ID AAW64261 standard; protein; 232 AA.  
DE Kallikrein substrate binding site.  
PN WO9824886-A1.  
PD 11-JUN-1998.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 38.1%; Score 524; DB 2; Length 232;  
Best Local Similarity 43.6%; Pred. No. 1.6e-32;  
RESULT 1194  
ID ABB84423 standard; peptide; 249 AA.  
DE Murine SCCE protein N-terminal fragment SEQ ID 50.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 38.0%; Score 521.5; DB 5; Length 249;  
Best Local Similarity 43.0%; Pred. No. 2.6e-32;  
RESULT 1195  
ID ABR96164 standard; protein; 261 AA.  
DE Human NOV13a protein SEQ ID NO:70.  
PN WO200290568-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.8%; Score 519.5; DB 6; Length 261;  
Best Local Similarity 40.0%; Pred. No. 3.9e-32;  
RESULT 1196  
ID ADL15205 standard; protein; 232 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 37.8%; Score 519; DB 7; Length 232;  
Best Local Similarity 44.5%; Pred. No. 3.8e-32;  
RESULT 1197  
ID ABG70276 standard; protein; 247 AA.  
DE Human Serine Protease TLSP-like protein.  
PN WO200255702-A2.  
PD 18-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 37.6%; Score 516; DB 5; Length 247;  
Best Local Similarity 42.5%; Pred. No. 6.9e-32;  
RESULT 1198

ID AAW94493 standard; protein; 268 AA.  
DE Human kallikrein.  
PN WO9842849-A1.  
PD 01-OCT-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 37.4%; Score 514; DB 2; Length 268;  
Best Local Similarity 46.4%; Pred. No. 1.1e-31;  
RESULT 1199  
ID ABB04645 standard; protein; 241 AA.  
DE Engraulis japonicus trypsinogen (atry II) SEQ ID NO:2.  
PN JP2001269173-A.  
PD 02-OCT-2001.  
PA (NISB ) JAPAN TOBACCO INC.  
Query Match 36.7%; Score 504; DB 5; Length 241;  
Best Local Similarity 45.9%; Pred. No. 5.6e-31;  
RESULT 1200  
ID AAU87693 standard; protein; 247 AA.  
DE Human pancreatic tumour protein #5.  
PN WO200212331-A2.  
PD 14-FEB-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.5%; Score 501; DB 5; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1201  
ID ADN04140 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #265.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1202  
ID ADN99594 standard; protein; 247 AA.  
DE Novel human protein sequence #410.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1203  
ID ADQ30589 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin II precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 36.5%; Score 501; DB 8; Length 247;  
Best Local Similarity 43.3%; Pred. No. 9.8e-31;  
RESULT 1204  
ID ABR41530 standard; protein; 261 AA.  
DE Human DITHP protein modification/maintenance protein.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 36.5%; Score 501; DB 6; Length 261;  
Best Local Similarity 43.3%; Pred. No. 1e-30;  
RESULT 1205  
ID AAB03862 standard; protein; 223 AA.  
DE Human neurosin amino acid sequence.  
PN WO200031284-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 36.4%; Score 500; DB 3; Length 223;  
Best Local Similarity 43.5%; Pred. No. 1.1e-30;  
RESULT 1206  
ID AAB21294 standard; protein; 254 AA.  
DE Human KLK-L1 protein #2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 498; DB 3; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1207

ID AAM01174 standard; protein; 254 AA.  
DE Human prostate-specific amino acid sequence P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1208  
ID AAU69819 standard; protein; 254 AA.  
DE Human prostate cDNA encoded protein #27.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1209  
ID AAG99059 standard; protein; 254 AA.  
DE Human prostate-specific amino acid of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1210  
ID ABU71710 standard; protein; 254 AA.  
DE Prostate cancer specific antigen P703P #7.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.2%; Score 498; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1211  
ID ABB95279 standard; protein; 254 AA.  
DE Human P703P putative full length protein SEQ ID NO 525.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.

PA (HEND/) HENDERSON R A.  
Query Match 36.2%; Score 498; DB 5; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1212  
ID ABP54360 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:13.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Query Match 36.2%; Score 498; DB 6; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1213  
ID ABP54357 standard; protein; 254 AA.  
DE Human KLK4 protein SEQ ID NO:6.  
PN WO200277243-A1.  
PD 03-OCT-2002.  
PA (UYQU-) UNIV QUEENSLAND TECHNOLOGY.  
Query Match 36.2%; Score 498; DB 6; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1214  
ID ABR54391 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 525.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 6; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1215  
ID ADB13975 standard; protein; 254 AA.  
DE Human prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 7; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1216  
ID ADG26391 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #60.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 7; Length 254;  
Best Local Similarity 43.1%; Pred. No. 1.7e-30;  
RESULT 1217  
ID AAB74830 standard; protein; 1079 AA.  
DE Prostate tumour antigen amino acid sequence for a fusion protein.  
PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 498; DB 4; Length 1079;  
Best Local Similarity 43.1%; Pred. No. 7.6e-30;  
RESULT 1218  
ID ABU71860 standard; protein; 1079 AA.  
DE Prostate specific antigen fusion protein #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.

PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.2%; Score 498; DB 4; Length 1079;  
Best Local Similarity 43.1%; Pred. No. 7.6e-30;  
RESULT 1219  
ID ADI17268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.2%; Score 497.5; DB 5; Length 230;  
Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
RESULT 1220  
ID ADI17276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.2%; Score 497.5; DB 5; Length 230;  
Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
RESULT 1221  
ID ADJ83075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LIL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 36.2%; Score 497.5; DB 7; Length 230;  
Best Local Similarity 47.4%; Pred. No. 1.7e-30;  
RESULT 1222  
ID ADL27345 standard; peptide; 280 AA.  
DE Amino acid sequence of trypsinogen.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 280;  
Best Local Similarity 42.7%; Pred. No. 2.1e-30;  
RESULT 1223  
ID ADL27346 standard; peptide; 461 AA.  
DE Amino acid sequence of trypsinogen-0aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 461;

Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1224  
ID ADL27347 standard; peptide; 464 AA.  
DE Amino acid sequence of trypsinogen-3aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 464;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1225  
ID ADL27348 standard; peptide; 485 AA.  
DE Amino acid sequence of trypsinogen-20aa-sp55.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEY/) AFEYAN N B.  
Query Match 36.2%; Score 497.5; DB 8; Length 485;  
Best Local Similarity 42.7%; Pred. No. 3.6e-30;  
RESULT 1226  
ID AAB21307 standard; protein; 249 AA.  
DE Human prostate.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 497; DB 3; Length 249;  
Best Local Similarity 43.1%; Pred. No. 2e-30;  
RESULT 1227  
ID AAB21320 standard; protein; 254 AA.  
DE Human prostate.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 36.2%; Score 497; DB 3; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1228  
ID AAY72525 standard; protein; 254 AA.  
DE Human prostate antigen #3.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 36.2%; Score 497; DB 4; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1229  
ID AAU74901 standard; protein; 254 AA.  
DE Protein sequence of prostate homologue #3.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.2%; Score 497; DB 5; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1230  
ID AAU74932 standard; protein; 254 AA.  
DE Amino acid sequence of prostate protein fragment #3.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.2%; Score 497; DB 5; Length 254;  
Best Local Similarity 43.1%; Pred. No. 2.1e-30;  
RESULT 1231  
ID AAW60592 standard; protein; 248 AA.  
DE Human prostate-specific kallikrein (HPSK) protein.  
PN WO9820117-A1.  
PD 14-MAY-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 36.1%; Score 496.5; DB 2; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1232  
ID AAY72524 standard; protein; 248 AA.  
DE Human prostate antigen #2.  
PN WO200104143-A2.  
PD 18-JAN-2001.

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 36.1%; Score 496.5; DB 4; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1233  
ID AAU74770 standard; protein; 248 AA.  
DE Protein sequence of prostate homologue #2.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.1%; Score 496.5; DB 5; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1234  
ID AAU74931 standard; protein; 248 AA.  
DE Amino acid sequence of prostate protein fragment #2.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 36.1%; Score 496.5; DB 5; Length 248;  
Best Local Similarity 43.4%; Pred. No. 2.2e-30;  
RESULT 1235  
ID ABG76997 standard; protein; 262 AA.  
DE Human kallikrein protein variant #1.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 36.0%; Score 495; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3e-30;  
RESULT 1236  
ID ADR90673 standard; protein; 246 AA.  
DE Human trypsinogen partial protein.  
PN WO2004078777-A2.  
PD 16-SEP-2004.  
PA (BIOR-) BIOREXIS PHARM CORP.  
Query Match 36.0%; Score 494.5; DB 8; Length 246;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1237  
ID AAB21321 standard; protein; 247 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 36.0%; Score 494.5; DB 3; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1238  
ID ABR54239 standard; protein; 247 AA.  
DE Human NOV35a protein SEQ ID NO:146.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.0%; Score 494.5; DB 6; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1239  
ID ABR54241 standard; protein; 247 AA.  
DE Human NOV35c protein SEQ ID NO:150.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 36.0%; Score 494.5; DB 6; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1240  
ID ADQ30588 standard; protein; 247 AA.  
DE Pancreas cancer marker - trypsin I precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 36.0%; Score 494.5; DB 8; Length 247;  
Best Local Similarity 41.9%; Pred. No. 3.1e-30;  
RESULT 1241  
ID AAM01173 standard; protein; 254 AA.



DE Human prostate-specific amino acid mature form of P703P.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1242  
ID AAU69818 standard; protein; 254 AA.  
DE Human prostate CDNA encoded protein #26.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1243  
ID AAG99058 standard; protein; 254 AA.  
DE Human prostate-specific mature protein of P703P.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1244  
ID ABU71709 standard; protein; 254 AA.  
DE Prostate cancer associated protein #12.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DEAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 36.0%; Score 494; DB 4; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1245  
ID ABB95278 standard; protein; 254 AA.  
DE Human P703P mature protein SEQ ID NO 523.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.

Query Match 36.0%; Score 494; DB 5; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1246  
ID ABR54390 standard; protein; 254 AA.  
DE Prostate tumour specific protein sequence SEQ ID 523.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 6; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1247  
ID ADB13973 standard; protein; 254 AA.  
DE Human mature prostate specific protein P703P.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1248  
ID ADG26389 standard; protein; 254 AA.  
DE Human prostate-specific polypeptide #59.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 36.0%; Score 494; DB 7; Length 254;  
Best Local Similarity 42.7%; Pred. No. 3.5e-30;  
RESULT 1249  
ID AAB21319 standard; protein; 262 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN) MOUNT SINAI HOSPITAL.  
Query Match 36.0%; Score 494; DB 3; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1250  
ID ABG76996 standard; protein; 262 AA.  
DE Human kallikrein protein.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 36.0%; Score 494; DB 5; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1251  
ID ADL15197 standard; protein; 262 AA.  
DE Human pancreatic kallikrein.  
PN CNI384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 36.0%; Score 494; DB 7; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1252  
ID ADL64969 standard; protein; 262 AA.  
DE Human kallikrein protein (KLK1).  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUIL/) HUI L.  
PA (PERR/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERB/) ZERBA K.  
Query Match 36.0%; Score 494; DB 8; Length 262;  
Best Local Similarity 40.4%; Pred. No. 3.6e-30;  
RESULT 1253  
ID ADQ39654 standard; protein; 262 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1317.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Query Match  
Best Local Similarity 36.0%; Score 494; DB 8; Length 262;  
RESULT 1254  
ID ADS34891 standard; protein; 262 AA.  
DE Human autoimmune disease-related protein - SEQ ID 105.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 36.0%; Score 494; DB 8; Length 262;  
RESULT 1255  
ID ABR54277 standard; protein; 240 AA.  
DE Human trypsinogen protein SEQ ID NO:341.  
PN WO2003023001-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 35.9%; Score 493.5; DB 6; Length 240;  
RESULT 1256  
ID AAB21316 standard; protein; 241 AA.  
DE Human trypsinogen.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 35.9%; Score 493.5; DB 3; Length 241;  
RESULT 1257  
ID ADN04297 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #343.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 8; Length 247;  
RESULT 1258  
ID AAB21308 standard; protein; 253 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 3; Length 253;  
RESULT 1259  
ID AAB21324 standard; protein; 258 AA.  
DE Human EMSP.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 3; Length 258;  
RESULT 1260  
ID AAW71005 standard; protein; 262 AA.  
DE Human prostate-associated kallikrein designated HPAK.  
PN WO9832865-A1.  
PD 30-JUL-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 2; Length 262;  
RESULT 1261  
ID ABP74711 standard; protein; 262 AA.  
DE Human glandular kallikrein 1 precursor protein SEQ ID NO:600.  
PN WO200281646-A2.  
PD 17-OCT-2002.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 6; Length 262;  
RESULT 1262  
ID ADL15204 standard; protein; 262 AA.  
DE Pancreatic kallikrein #1.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 7; Length 262;

Best Local Similarity 40.4%; Pred. No. 4.3e-30;  
RESULT 1263  
ID ADM72846 standard; protein; 263 AA.  
DE Human glandular kallikrein 1 protein SEQ ID NO:105.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Query Match  
Best Local Similarity 35.9%; Score 493; DB 8; Length 263;  
RESULT 1264  
ID AAB98503 standard; protein; 225 AA.  
DE Human trypsin serine protease catalytic domain.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 4; Length 225;  
RESULT 1265  
ID AAW93488 standard; protein; 230 AA.  
DE Human TRYI trypsinogen variant protein.  
PN WO910503-A1.  
PD 04-MAR-1999.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 2; Length 230;  
RESULT 1266  
ID AAB21315 standard; protein; 256 AA.  
DE Human KLK1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 3; Length 256;  
RESULT 1267  
ID AAP95121 standard; protein; 262 AA.  
DE Kallikrein encoded by clone lambda HK65a.  
PN EP297913-A.  
PD 04-JAN-1989.  
PA (AMGE-) AMGEN.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 1; Length 262;  
RESULT 1268  
ID ABG76998 standard; protein; 262 AA.  
DE Human kallikrein protein variant #2.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 5; Length 262;  
RESULT 1269  
ID AAB54293 standard; protein; 267 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:745.  
PN WO200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 35.8%; Score 492; DB 3; Length 267;  
RESULT 1270  
ID ABG77002 standard; protein; 262 AA.  
DE Human kallikrein 1 polymorphic sequence.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match  
Best Local Similarity 35.7%; Score 491; DB 5; Length 262;  
RESULT 1271  
ID ADA05744 standard; protein; 224 AA.  
DE Human NOV18g protein SEQ ID NO:104.  
PN WO2003029424-A2.

PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP. 35.7%; Score 490; DB 6; Length 224;  
Query Match 45.3%; Pred. No. 6.3e-30;  
Best Local Similarity 45.3%; Pred. No. 6.3e-30;  
RESULT 1272  
ID ADN62908 standard; protein; 224 AA.  
DE Human NOV189.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGE E M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 35.7%; Score 490; DB 8; Length 224;  
Best Local Similarity 45.3%; Pred. No. 6.3e-30;  
RESULT 1273  
ID AAE00397 standard; protein; 234 AA.  
DE Human serine protease, PROST 07.  
PN WO200125446-A1.  
PD 12-APR-2001.  
PA (SCHD ) SCHERING AG. 35.6%; Score 489.5; DB 4; Length 234;  
Query Match 43.0%; Pred. No. 7.2e-30;  
Best Local Similarity 43.0%; Pred. No. 7.2e-30;  
RESULT 1274  
ID AAY25510 standard; protein; 231 AA.  
DE Human prostate serine protease protein.  
PN EP936270-A2.  
PD 18-AUG-1999.  
PA (BADI ) BASF AG. 35.6%; Score 488.5; DB 2; Length 231;  
Query Match 43.9%; Pred. No. 8.4e-30;  
Best Local Similarity 43.9%; Pred. No. 8.4e-30;  
RESULT 1275  
ID ADN04726 standard; protein; 247 AA.  
DE Antipsoriatic protein sequence #544.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC. 35.5%; Score 488; DB 8; Length 247;  
Query Match 42.3%; Pred. No. 9.9e-30;  
Best Local Similarity 42.3%; Pred. No. 9.9e-30;  
RESULT 1276  
ID ADN99593 standard; protein; 247 AA.  
DE Novel human protein sequence #409.  
PN WO2004038003-A2.

PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. 35.5%; Score 488; DB 8; Length 247;  
Query Match 42.3%; Pred. No. 9.9e-30;  
Best Local Similarity 42.3%; Pred. No. 9.9e-30;  
RESULT 1277  
ID AAM01227 standard; protein; 449 AA.  
DE P703P and PSA fusion amino acid sequence.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
Query Match 44.1%; Pred. No. 2e-29;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1278  
ID AAU69872 standard; protein; 449 AA.  
DE Human prostate serum antigen/p703P fusion protein.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP. 35.5%; Score 487.5; DB 4; Length 449;  
Query Match 44.1%; Pred. No. 2e-29;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1279  
ID ABU71763 standard; protein; 449 AA.  
DE Prostate cancer specific antigen fusion protein #1.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1280  
ID ABB95332 standard; protein; 449 AA.  
DE Human P703P/PSA fusion protein SEQ ID NO 617.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
Query Match 35.5%; Score 487.5; DB 5; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;

RESULT 1281  
ID ABR54444 standard; protein; 449 AA.  
DE Prostate tumour specific protein sequence SEQ ID 617.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 6; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1282  
ID ADB14067 standard; protein; 449 AA.  
DE Human prostate specific protein P703P/PSA fusion protein.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1283  
ID ADG26483 standard; protein; 449 AA.  
DE Human prostate-specific polypeptide #113.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 449;  
Best Local Similarity 44.1%; Pred. No. 2e-29;  
RESULT 1284  
ID ABU71889 standard; protein; 585 AA.  
DE Prostate cancer specific antigen fusion protein #3.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1285  
ID ABU71888 standard; protein; 585 AA.  
DE Prostate cancer associated protein #72.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1286  
ID ABR54580 standard; protein; 585 AA.  
DE Prostate tumour-related protein SEQ ID 1020.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 6; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1287  
ID ADB14470 standard; protein; 585 AA.  
DE FOPP/hPAP fusion protein, FOPP3.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1288  
ID ADG26993 standard; protein; 585 AA.  
DE Human prostate-specific polypeptide #249.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1289  
ID ABU71890 standard; protein; 801 AA.  
DE Prostate cancer specific antigen fusion protein #4.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 801;  
Best Local Similarity 44.1%; Pred. No. 3.6e-29;  
RESULT 1290  
ID AAY31160 standard; protein; 224 AA.  
DE Human trypsin serine protease protein domain.  
PN US5948892-A.  
PD 07-SEP-1999.  
PA (AMGE-) AMGEN INC.  
Query Match 35.4%; Score 487; DB 2; Length 224;  
Best Local Similarity 43.4%; Pred. No. 1.1e-29;  
RESULT 1291  
ID ADL15207 standard; protein; 261 AA.  
DE Pancreatic kallikrein #3.

PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1286  
ID ABR54580 standard; protein; 585 AA.  
DE Prostate tumour-related protein SEQ ID 1020.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 6; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1287  
ID ADB14470 standard; protein; 585 AA.  
DE FOPP/hPAP fusion protein, FOPP3.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1288  
ID ADG26993 standard; protein; 585 AA.  
DE Human prostate-specific polypeptide #249.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 35.5%; Score 487.5; DB 7; Length 585;  
Best Local Similarity 44.1%; Pred. No. 2.6e-29;  
RESULT 1289  
ID ABU71890 standard; protein; 801 AA.  
DE Prostate cancer specific antigen fusion protein #4.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 35.5%; Score 487.5; DB 4; Length 801;  
Best Local Similarity 44.1%; Pred. No. 3.6e-29;  
RESULT 1290  
ID AAY31160 standard; protein; 224 AA.  
DE Human trypsin serine protease protein domain.  
PN US5948892-A.  
PD 07-SEP-1999.  
PA (AMGE-) AMGEN INC.  
Query Match 35.4%; Score 487; DB 2; Length 224;  
Best Local Similarity 43.4%; Pred. No. 1.1e-29;  
RESULT 1291  
ID ADL15207 standard; protein; 261 AA.  
DE Pancreatic kallikrein #3.



PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.3%; Score 484.5; DB 7; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.9e-29;  
RESULT 1292  
ID ABM83249 standard; protein; 261 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3498.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 261;  
Best Local Similarity 43.5%; Pred. No. 2.1e-29;  
RESULT 1293  
ID ABM83250 standard; protein; 333 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3499.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 35.2%; Score 484; DB 8; Length 333;  
Best Local Similarity 43.5%; Pred. No. 2.7e-29;  
RESULT 1294  
ID AAW57740 standard; protein; 240 AA.  
DE Trypsinogen-like protein.  
PN JP10099080-A.  
PD 21-APR-1998.  
PA (SHIS ) SHISEIDO CO LTD.  
Query Match 35.2%; Score 483.5; DB 2; Length 240;  
Best Local Similarity 42.5%; Pred. No. 2.1e-29;  
RESULT 1295  
ID ADL15206 standard; protein; 260 AA.  
DE Pancreatic kallikrein #2.  
PN CN1384199-A.  
PD 11-DEC-2002.  
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.  
Query Match 35.2%; Score 483; DB 7; Length 260;  
Best Local Similarity 39.8%; Pred. No. 2.5e-29;  
RESULT 1296  
ID AAB21293 standard; protein; 237 AA.  
DE Human KLK-L1 protein #1.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 35.1%; Score 482.5; DB 3; Length 237;  
Best Local Similarity 42.2%; Pred. No. 2.5e-29;  
RESULT 1297  
ID AAP70568 standard; protein; 262 AA.  
DE Human kallikrein-like substance has hypotensive activity.  
PN JP62126980-A.  
PD 09-JUN-1987.  
PA (NAKA/) NAKANISHI S.  
Query Match 35.0%; Score 481; DB 1; Length 262;  
Best Local Similarity 40.0%; Pred. No. 3.6e-29;  
RESULT 1298  
ID AAU01290 standard; protein; 216 AA.  
DE Human serine protease HETAA37p.  
PN WO200123587-A2.  
PD 05-APR-2001.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 34.8%; Score 477.5; DB 4; Length 216;  
Best Local Similarity 44.3%; Pred. No. 5.5e-29;  
RESULT 1299  
ID AAY72526 standard; protein; 226 AA.  
DE Human prostate antigen P703PDE5 sequence.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1300  
ID AAU74902 standard; protein; 226 AA.  
DE Protein sequence of prostate homologue #4.

PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1301  
ID AAU74933 standard; protein; 226 AA.  
DE Amino acid sequence of prostate protein fragment #4.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 226;  
Best Local Similarity 43.8%; Pred. No. 5.8e-29;  
RESULT 1302  
ID AAY72522 standard; protein; 312 AA.  
DE NS1-P703P-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.8%; Score 477.5; DB 4; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1303  
ID AAU74768 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NS1-p703-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1304  
ID AAU74929 standard; protein; 312 AA.  
DE Amino acid sequence of wild-type NS1-P703P-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.8%; Score 477.5; DB 5; Length 312;  
Best Local Similarity 43.8%; Pred. No. 8.1e-29;  
RESULT 1305  
ID ABU71886 standard; protein; 344 AA.  
DE Human prostate specific antigen (PSA) epitope #26.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DEAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match 34.8%; Score 477.5; DB 4; Length 344;  
Best Local Similarity 43.8%; Pred. No. 8.9e-29;  
RESULT 1306  
ID ABM82601 standard; protein; 239 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2850.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.



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PN US2003157089-A1.
PD 21-AUG-2003.
PA (CORI-) CORIXA CORP. 34.4%; Score 472.5; DB 7; Length 220;
Query Match 34.4%; Score 472.5; DB 7; Length 220;
Best Local Similarity 43.8%; Pred. No. 1.4e-28;
RESULT 1321
ID ADI39732 standard; protein; 262 AA.
DE Human glandular kallikrein (HK2) protein.
PN US6642013-B1.
PD 04-NOV-2003.
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI. 34.4%; Score 472.5; DB 8; Length 262;
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
RESULT 1322
ID ADI37156 standard; protein; 262 AA.
DE Human glandular kallikrein (hHK2) protein.
PN US2003199010-A1.
PD 23-OCT-2003.
PA (UYAR-) UNIV ARKANSAS. 34.4%; Score 472.5; DB 8; Length 262;
Query Match 34.4%; Score 472.5; DB 8; Length 262;
Best Local Similarity 38.9%; Pred. No. 1.6e-28;
RESULT 1323
ID ABR96163 standard; protein; 274 AA.
DE Human NOV12a protein SEQ ID NO:68.
PN WO200290568-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP. 34.4%; Score 472.5; DB 6; Length 274;
Query Match 34.4%; Score 472.5; DB 6; Length 274;
Best Local Similarity 40.7%; Pred. No. 1.7e-28;
RESULT 1324
ID AAP92314 standard; protein; 245 AA.
DE Human recombinant kallikrein gene.
PN EP297913-A.
PD 04-JAN-1989.
PA (AMGE-) AMGEN. 34.3%; Score 471; DB 1; Length 245;
Query Match 34.3%; Score 471; DB 1; Length 245;
Best Local Similarity 40.2%; Pred. No. 2e-28;
RESULT 1325
ID AAB21313 standard; protein; 255 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL. 34.2%; Score 470.5; DB 3; Length 255;
Query Match 34.2%; Score 470.5; DB 3; Length 255;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1326
ID AAU06276 standard; protein; 257 AA.
DE Prostate specific Antigen (PSA) polypeptide.
PN WO200145728-A2.
PD 28-JUN-2001.
PA (EPIM-) EPIMUNE INC. 34.2%; Score 470.5; DB 4; Length 257;
Query Match 34.2%; Score 470.5; DB 4; Length 257;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1327
ID AAW13649 standard; protein; 261 AA.
DE Human prostatic specific antigen.
PN WO9711172-A1.
PD 27-MAR-1997.
PA (WORC-) WORCESTER FOUND BIOMEDICAL RES. 34.2%; Score 470.5; DB 2; Length 261;
Query Match 34.2%; Score 470.5; DB 2; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1328
ID AAY56048 standard; protein; 261 AA.
DE Human prostate-specific antigen.
PN WO9961068-A1.
PD 02-DEC-1999.
PA (UYPE-) UNIV PENNSYLVANIA. 34.2%; Score 470.5; DB 3; Length 261;
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1329
ID AAY77842 standard; protein; 261 AA.
DE Human prostate-specific antigen (PSA) sequence.
PN WO9960984-A2. 34.2%; Score 470.5; DB 6; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;

PD 02-DEC-1999.
PA (ENTR-) ENTREMED INC. 34.2%; Score 470.5; DB 3; Length 261;
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1330
ID AAB21317 standard; protein; 261 AA.
DE Human PSA.
PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN ) MOUNT SINAI HOSPITAL. 34.2%; Score 470.5; DB 3; Length 261;
Query Match 34.2%; Score 470.5; DB 3; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1331
ID AAB74821 standard; protein; 261 AA.
DE Prostate tumour antigen amino acid sequence for PSA.
PN WO200125272-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP. 34.2%; Score 470.5; DB 4; Length 261;
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1332
ID AAG62144 standard; protein; 261 AA.
DE Human prostate specific membrane antigen SEQ ID NO: 327.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP. 34.2%; Score 470.5; DB 4; Length 261;
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1333
ID AAG62146 standard; protein; 261 AA.
DE Human prostate specific antigen SEQ ID NO: 329.
PN WO200125273-A2.
PD 12-APR-2001.
PA (CORI-) CORIXA CORP. 34.2%; Score 470.5; DB 4; Length 261;
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1334
ID ABU71859 standard; protein; 261 AA.
DE Human prostatic specific membrane antigen (PSMA).
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J. 34.2%; Score 470.5; DB 4; Length 261;
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1335
ID ABU71859 standard; protein; 261 AA.
DE Human prostatic specific membrane antigen (PSMA).
PN US2002192763-A1.
PD 19-DEC-2002.
PA (XUJJ/) XU J. 34.2%; Score 470.5; DB 4; Length 261;
Query Match 34.2%; Score 470.5; DB 4; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1335
ID ABP74202 standard; protein; 261 AA.
DE Human PSA protein SEQ ID NO:78.
PN WO200281646-A2.
PD 17-OCT-2002.
PA (CTLI-) CTL IMMUNOTHERAPIES CORP. 34.2%; Score 470.5; DB 6; Length 261;
Query Match 34.2%; Score 470.5; DB 6; Length 261;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
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RESULT 1336  
ID ADB82777 standard; protein; 261 AA.  
DE Human protein sequence useful for the treatment of cancer (SeqID 1558).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1337  
ID ADC09580 standard; protein; 261 AA.  
DE PSA protein #SEQ ID 78.  
PN WO2003008537-A2.  
PD 30-JAN-2003.  
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1338  
ID ADJ59022 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.2%; Score 470.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1339  
ID ADI39733 standard; protein; 261 AA.  
DE Human prostate specific antigen (PSA) protein.  
PN US6642013-B1.  
PD 04-NOV-2003.  
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1340  
ID ADI37157 standard; protein; 261 AA.  
DE Human prostate specific antigen (hPSA).  
PN US2003199010-A1.  
PD 23-OCT-2003.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1341  
ID ADM72819 standard; protein; 261 AA.  
DE Human PSA protein SEQ ID NO:78.  
PN WO2004022709-A2.  
PD 18-MAR-2004.  
PA (MANN-) MANNKIND CORP.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1342  
ID ABM82166 standard; protein; 261 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 34.2%; Score 470.5; DB 8; Length 261;  
Best Local Similarity 40.4%; Pred. No. 2.3e-28;  
RESULT 1343  
ID AAB08449 standard; protein; 375 AA.  
DE A human prostate specific antigen variant polypeptide.  
PN WO200049158-A2.  
PD 24-AUG-2000.  
PA (COMP-) COMPUGEN LTD.  
Query Match 34.2%; Score 470.5; DB 3; Length 375;  
Best Local Similarity 40.4%; Pred. No. 3.4e-28;  
RESULT 1344  
ID AAG62154 standard; protein; 692 AA.  
DE Human WT1/PSA fusion protein SEQ ID NO: 357.  
PN WO200125273-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 34.2%; Score 470.5; DB 4; Length 692;  
Best Local Similarity 40.4%; Pred. No. 6.3e-28;

RESULT 1345  
ID AAB67545 standard; protein; 284 AA.  
DE Amino acid sequence of protease MH2 catalytic domain in PFEK2-6XHIS-TAG.  
PN WO200116289-A2.  
PD 08-MAR-2001.  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
Query Match 34.1%; Score 469; DB 4; Length 284;  
Best Local Similarity 43.8%; Pred. No. 3.3e-28;  
RESULT 1346  
ID ADJ59024 standard; protein; 261 AA.  
DE Human PSA precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.1%; Score 468.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 3.3e-28;  
RESULT 1347  
ID AAU74903 standard; protein; 231 AA.  
DE Amino acid sequence of p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1348  
ID AAU74934 standard; protein; 231 AA.  
DE Amino acid sequence of P703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 231;  
Best Local Similarity 43.4%; Pred. No. 3.5e-28;  
RESULT 1349  
ID AAY72521 standard; protein; 312 AA.  
DE NS1-P703P mutated-His fusion protein.  
PN WO200104143-A2.  
PD 18-JAN-2001.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 34.0%; Score 467.5; DB 4; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1350  
ID AAU74767 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-p703 mutated-His fusion protein.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1351  
ID AAU74928 standard; protein; 312 AA.  
DE Amino acid sequence of NS1-P703P mutated-His fusion protein.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 34.0%; Score 467.5; DB 5; Length 312;  
Best Local Similarity 43.4%; Pred. No. 4.8e-28;  
RESULT 1352  
ID AAP81243 standard; protein; 247 AA.  
DE Human spleen trypsin III (trypsinogen III).  
PN JP63160582-A.  
PD 04-JUL-1988.  
PA (SANY ) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 1; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;  
RESULT 1353  
ID AAR82703 standard; protein; 247 AA.  
DE Human pancreatic trypsin III.  
PN JP07184655-A.  
PD 25-JUL-1995.  
PA (SANY ) SANKYO CO LTD.  
Query Match 34.0%; Score 467; DB 2; Length 247;  
Best Local Similarity 40.9%; Pred. No. 4.1e-28;



RESULT 1354  
ID ADJ59026 standard; protein; 261 AA.  
DE Human PSA analogue (Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 34.0%; Score 466.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 4.7e-28;  
RESULT 1355  
ID ABB84422 standard; peptide; 226 AA.  
DE Rat SCCE protein N-terminal fragment SEQ ID 48.  
PN WO200262135-A2.  
PD 15-AUG-2002.  
PA (EGEL/) EGELRUD T.  
PA (HANS/) HANSSON L.  
Query Match 33.8%; Score 464.5; DB 5; Length 226;  
Best Local Similarity 42.7%; Pred. No. 5.8e-28;  
RESULT 1356  
ID ADJ59028 standard; protein; 261 AA.  
DE Human PSA analogue (L155/Y154) precursor protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.8%; Score 464.5; DB 7; Length 261;  
Best Local Similarity 40.4%; Pred. No. 6.8e-28;  
RESULT 1357  
ID ADA50549 standard; protein; 237 AA.  
DE Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.8%; Score 464; DB 6; Length 237;  
Best Local Similarity 42.6%; Pred. No. 6.7e-28;  
RESULT 1358  
ID ADM12395 standard; protein; 261 AA.  
DE Human prostate-specific antigen protein.  
PN US2003235594-A1.  
PD 25-DEC-2003.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Query Match 33.7%; Score 463.5; DB 8; Length 261;  
Best Local Similarity 40.0%; Pred. No. 8.1e-28;  
RESULT 1359  
ID ADR66838 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 131 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1360  
ID ADR66277 standard; protein; 248 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 131 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 248;  
Best Local Similarity 40.2%; Pred. No. 9.2e-28;  
RESULT 1361  
ID ADR66934 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 232 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1362  
ID ADR66036 standard; protein; 251 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 232 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 33.7%; Score 462.5; DB 8; Length 251;  
Best Local Similarity 40.2%; Pred. No. 9.3e-28;  
RESULT 1363  
ID ADR27546 standard; protein; 281 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 281;  
Best Local Similarity 41.0%; Pred. No. 1.1e-27;  
RESULT 1364  
ID ADP27545 standard; protein; 297 AA.  
DE Human kallikrein-3 (KLK-3) EHT103 protien a variant SeqID 19.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 33.6%; Score 462; DB 8; Length 297;  
Best Local Similarity 41.0%; Pred. No. 1.2e-27;  
RESULT 1365  
ID AAR84668 standard; protein; 261 AA.  
DE Prepro-hK2 kallikrein.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1366  
ID AAW10600 standard; protein; 261 AA.  
DE Human prepro-Trp226-glandular kallikrein-2.  
PN WO9701630-A1.  
PD 16-JAN-1997.  
PA (ORIN ) ORION YHTYMAE OY.  
Query Match 33.5%; Score 460.5; DB 2; Length 261;  
Best Local Similarity 40.2%; Pred. No. 1.4e-27;  
RESULT 1367  
ID AAU98921 standard; protein; 245 AA.  
DE Human prostate specific antigen (PSA) variant.  
PN WO200240059-A2.  
PD 23-MAY-2002.  
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.  
PA (MINC/) MINCHEFF M S.  
PA (LOUK/) LOUKINOV D I.  
PA (ZOUB/) ZOUBAK S.  
Query Match 33.4%; Score 459.5; DB 5; Length 245;  
Best Local Similarity 41.4%; Pred. No. 1.5e-27;  
RESULT 1368  
ID AAY08894 standard; protein; 238 AA.  
DE Chimeric serine protease FXT protein.  
PN EP927764-A2.  
PD 07-JUL-1999.  
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
Query Match 33.4%; Score 459; DB 2; Length 238;  
Best Local Similarity 40.5%; Pred. No. 1.6e-27;  
RESULT 1369  
ID AAB21314 standard; protein; 255 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 255;  
Best Local Similarity 40.8%; Pred. No. 1.9e-27;  
RESULT 1370  
ID AAW06971 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein prepro-hK2.  
PN WO9634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITECH INC.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1371  
ID AAW83203 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein protein pphK2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1372  
ID AAW49085 standard; protein; 261 AA.  
DE Wild-type human Kallikrein 2 (hK2).  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1373  
ID AAW45397 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein precursor prepro-hK2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1374  
ID AAW96189 standard; protein; 261 AA.  
DE Prepro human Kallikrein 2 (preprohK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.4%; Score 458.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1375  
ID AAB21318 standard; protein; 261 AA.  
DE Human KLK2.  
PN WO200053776-A2.  
PD 14-SEP-2000.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 33.4%; Score 458.5; DB 3; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1376  
ID AAU06279 standard; protein; 261 AA.  
DE Human Kallikrein2 polypeptide.  
PN WO200145728-A2.  
PD 28-JUN-2001.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 33.4%; Score 458.5; DB 4; Length 261;  
Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1377  
ID ADB75390 standard; protein; 261 AA.  
DE Prostate cancer marker protein.  
PN WO2003009814-A2.  
PD 06-FEB-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 33.4%; Score 458.5; DB 7; Length 261;

Best Local Similarity 40.8%; Pred. No. 2e-27;  
RESULT 1378  
ID AAW83213 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hK3.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1379  
ID AAW56086 standard; protein; 237 AA.  
DE Human prostate specific antigen protein.  
PN WO9810292-A1.  
PD 12-MAR-1998.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1380  
ID AAW96187 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 33.3%; Score 457.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1381  
ID AAB11041 standard; peptide; 237 AA.  
DE Human prostate-specific antigen N-terminal fragment #2.  
PN EP1043394-A2.  
PD 11-OCT-2000.  
PA (SERA-) SERATEC GES BIOTECHNOLOGIE MBH.  
Query Match 33.3%; Score 457.5; DB 3; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1382  
ID AAB19819 standard; protein; 237 AA.  
DE Prostate specific antigen specific to benign prostatic hyperplasia.  
PN WO200067030-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1383  
ID AAB19818 standard; protein; 237 AA.  
DE Prostate specific antigen elevated in benign prostatic hyperplasia.  
PN WO200066718-A1.  
PD 09-NOV-2000.  
PA (HYBR-) HYBRITECH INC.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
Query Match 33.3%; Score 457.5; DB 4; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1384  
ID ADA50546 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1385  
ID ADA09840 standard; protein; 237 AA.  
DE Human mature prostate specific antigen (PSA).  
PN US2003059864-A1.  
PD 27-MAR-2003.  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (RITT/) RITTENHOUSE H G.  
Query Match 33.3%; Score 457.5; DB 6; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1386

ID ADJ59023 standard; protein; 237 AA.  
DE Human PSA mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.3%; Score 457.5; DB 7; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1387  
ID ADF60980 standard; protein; 237 AA.  
DE Human prostate specific antigen (PSA).  
PN US2003166036-A1.  
PD 04-SEP-2003.  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (RITT/) RITTENHOUSE H G.  
Query Match 33.3%; Score 457.5; DB 8; Length 237;  
Best Local Similarity 41.6%; Pred. No. 2.1e-27;  
RESULT 1388  
ID AAP70677 standard; protein; 245 AA.  
DE Human kallikrein gene product.  
PN WO8702709-A.  
PD 07-MAY-1987.  
PA (BIOT-) BIOTECHN RES PARTN.  
PA (CALB-) CALIF BIOTECHNOL INC.  
Query Match 33.2%; Score 456; DB 1; Length 245;  
Best Local Similarity 39.7%; Pred. No. 2.9e-27;  
RESULT 1389  
ID AAW45398 standard; protein; 237 AA.  
DE Prostate-specific antigen protein hK3 (PSA).  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.2%; Score 455.5; DB 2; Length 237;  
Best Local Similarity 41.6%; Pred. No. 3e-27;  
RESULT 1390  
ID ADJ59025 standard; protein; 237 AA.  
DE Human PSA mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.2%; Score 455.5; DB 7; Length 237;  
Best Local Similarity 41.6%; Pred. No. 3e-27;  
RESULT 1391  
ID AAW06972 standard; protein; 261 AA.  
DE Kallikrein prepro-hK2v217 variant.  
PN WO9634964-A2.  
PD 07-NOV-1996.  
PA (HYBR-) HYBRITECH INC.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 33.2%; Score 455.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 3.3e-27;  
RESULT 1392  
ID AAW45400 standard; protein; 261 AA.  
DE Prostate-specific glandular kallikrein hK2v217.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.2%; Score 455.5; DB 2; Length 261;  
Best Local Similarity 40.8%; Pred. No. 3.3e-27;  
RESULT 1393  
ID AAW59129 standard; protein; 232 AA.  
DE Homo sapiens Tub Interactor (hTI-1) protein.  
PN WO9812302-A1.  
PD 26-MAR-1998.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 33.1%; Score 454.5; DB 2; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1394  
ID AAY72523 standard; protein; 232 AA.  
DE Human prostate antigen #1.  
PN WO200104143-A2.  
PD 18-JAN-2001.

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA (CORI-) CORIXA CORP.  
Query Match 33.1%; Score 454.5; DB 4; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1395  
ID AAU74769 standard; protein; 232 AA.  
DE Protein sequence of prostate homologue #1.  
PN WO200200708-A2.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 33.1%; Score 454.5; DB 5; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1396  
ID AAU74930 standard; protein; 232 AA.  
DE Amino acid sequence of prostate protein fragment #1.  
PN WO200200867-A1.  
PD 03-JAN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
Query Match 33.1%; Score 454.5; DB 5; Length 232;  
Best Local Similarity 43.8%; Pred. No. 3.5e-27;  
RESULT 1397  
ID AAR84669 standard; protein; 244 AA.  
DE Pro-hK2 kallikrein.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 33.1%; Score 454.5; DB 2; Length 244;  
Best Local Similarity 41.2%; Pred. No. 3.7e-27;  
RESULT 1398  
ID ADO38617 standard; protein; 261 AA.  
DE Prostate Specific Antigen (PSA).  
PN US2004058881-A1.  
PD 25-MAR-2004.  
PA (ANTI-) ANTIGEN EXPRESS INC.  
Query Match 33.1%; Score 454.5; DB 8; Length 261;  
Best Local Similarity 39.6%; Pred. No. 4e-27;  
RESULT 1399  
ID ADJ59027 standard; protein; 237 AA.  
DE Human PSA analogue (Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 33.0%; Score 453.5; DB 7; Length 237;  
Best Local Similarity 41.6%; Pred. No. 4.3e-27;  
RESULT 1400  
ID AAW83204 standard; protein; 244 AA.  
DE Prostate-specific glandular kallikrein protein pHK2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;  
Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1401  
ID AAW45396 standard; protein; 244 AA.  
DE Prostate-specific glandular kallikrein precursor pro-hK2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;  
Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1402  
ID AAW96188 standard; protein; 244 AA.  
DE Pro.human Kallikrein 2 (prohK2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.9%; Score 452.5; DB 2; Length 244;

Best Local Similarity 41.8%; Pred. No. 5.3e-27;  
RESULT 1403  
ID AAW03130 standard; protein; 250 AA.  
DE Prostate-specific antigen.  
PN WO9621042-A2.  
PD 11-JUL-1996.  
PA (UYBO-) UNIV BOSTON.  
Query Match 32.9%; Score 452.5; DB 2; Length 250;  
Best Local Similarity 40.5%; Pred. No. 5.4e-27;  
RESULT 1404  
ID ADP27538 standard; protein; 281 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 281;  
Best Local Similarity 41.8%; Pred. No. 6.1e-27;  
RESULT 1405  
ID ADP27537 standard; protein; 297 AA.  
DE Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.  
PN FR2848569-A1.  
PD 18-JUN-2004.  
PA (EXON-) EXONHIT THERAPEUTICS SA.  
Query Match 32.9%; Score 452.5; DB 8; Length 297;  
Best Local Similarity 41.8%; Pred. No. 6.5e-27;  
RESULT 1406  
ID ADJ59029 standard; protein; 236 AA.  
DE Human PSA analogue (L155/Y154) mature protein sequence.  
PN WO2003047506-A2.  
PD 12-JUN-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 32.9%; Score 451.5; DB 7; Length 236;  
Best Local Similarity 41.6%; Pred. No. 6.1e-27;  
RESULT 1407  
ID AAR77098 standard; protein; 237 AA.  
DE Prostate-specific antigen.  
PN WO9528498-A1.  
PD 26-OCT-1995.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 40.7%; Pred. No. 7.4e-27;  
RESULT 1408  
ID AAW83202 standard; protein; 237 AA.  
DE Prostate-specific glandular kallikrein protein hK2.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1409  
ID AAW45395 standard; protein; 237 AA.  
DE Mature prostate-specific glandular kallikrein hK2.  
PN WO9802748-A1.  
PD 22-JAN-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1410  
ID AAW96186 standard; protein; 237 AA.  
DE Mature human Kallikrein 2 (hK2) .  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUN/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.8%; Score 450.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1411  
ID ADA50561 standard; protein; 237 AA.  
DE Kallikrein KLK2, SEQ ID NO:16.

PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Query Match 32.8%; Score 450.5; DB 6; Length 237;  
Best Local Similarity 42.0%; Pred. No. 7.4e-27;  
RESULT 1412  
ID AAR84667 standard; protein; 237 AA.  
DE Mature kallikrein hK2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.6%; Score 448.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1e-26;  
RESULT 1413  
ID ADI17277 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 813.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1414  
ID ADI17269 standard; protein; 217 AA.  
DE Polypeptide homologous to a human NOVX domain SeqID 805.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 32.6%; Score 447.5; DB 5; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1415  
ID ADJ83076 standard; protein; 217 AA.  
DE Trypsin protein which is related to human NOVX protein - SEQ ID 67.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHIMKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 32.6%; Score 447.5; DB 7; Length 217;  
Best Local Similarity 44.4%; Pred. No. 1.1e-26;  
RESULT 1416  
ID AAW83212 standard; protein; 237 AA.  
DE hK2 variant A217V.  
PN WO9846795-A1.  
PD 22-OCT-1998.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (MAYO-) MAYO FOUNDATION.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1417



ID AAW49087 standard; protein; 237 AA.  
DE Mutant human Kallikrein 2 (hk2) A217V.  
PN WO9821365-A2.  
PD 22-MAY-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1418  
ID AAW96190 standard; protein; 237 AA.  
DE Variant human Kallikrein 2 (hk2).  
PN WO9859073-A1.  
PD 30-DEC-1998.  
PA (MAYO-) MAYO FOUNDATION.  
PA (YOUNG/) YOUNG C Y F.  
PA (TIND/) TINDALL D J.  
PA (KLEE/) KLEE G G.  
Query Match 32.6%; Score 447.5; DB 2; Length 237;  
Best Local Similarity 42.0%; Pred. No. 1.3e-26;  
RESULT 1419  
ID AAW11023 standard; protein; 240 AA.  
DE Human prostate specific antigen.  
PN WO9640754-A1.  
PD 19-DEC-1996.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 32.4%; Score 445; DB 2; Length 240;  
Best Local Similarity 41.0%; Pred. No. 2e-26;  
RESULT 1420  
ID AAR84671 standard; protein; 237 AA.  
DE Mature kallikrein hk3.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.4%; Score 444.5; DB 2; Length 237;  
Best Local Similarity 41.1%; Pred. No. 2.1e-26;  
RESULT 1421  
ID ABM82643 standard; protein; 227 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2892.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 32.2%; Score 443; DB 8; Length 227;  
Best Local Similarity 39.6%; Pred. No. 2.7e-26;  
RESULT 1422  
ID AAR84670 standard; protein; 238 AA.  
DE Mature kallikrein hk2.  
PN WO9530758-A1.  
PD 16-NOV-1995.  
PA (MAYO-) MAYO FOUNDATION.  
PA (HYBR-) HYBRITECH INC.  
Query Match 32.1%; Score 441.5; DB 2; Length 238;  
Best Local Similarity 40.9%; Pred. No. 3.6e-26;  
RESULT 1423  
ID AAR94526 standard; protein; 279 AA.  
DE Korean Viper Salmo salar thrombin-like protease, Halybin.  
PN EP707067-A2.  
PD 17-APR-1996.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match 32.0%; Score 439; DB 2; Length 279;  
Best Local Similarity 37.7%; Pred. No. 6.7e-26;  
RESULT 1424  
ID AAG79000 standard; protein; 233 AA.  
DE Mamushi fibrinolytic enzyme, brevinase.  
PN KR2001045716-A.  
PD 05-JUN-2001.  
PA (LEEJ/) LEE J W.  
PA (PARK/) PARK W.  
Query Match 31.8%; Score 436.5; DB 4; Length 233;  
Best Local Similarity 37.9%; Pred. No. 8.7e-26;  
RESULT 1425  
ID AAM52944 standard; protein; 260 AA.  
DE Agkistrodon halys brevicaudus thrombin-like protease, salmabin.

PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 31.7%; Score 436; DB 2; Length 260;  
Best Local Similarity 36.1%; Pred. No. 1.1e-25;  
RESULT 1426  
ID AAB50447 standard; protein; 205 AA.  
DE Human prostate cancer-related intracellular protein #1.  
PN WO200071711-A2.  
PD 30-NOV-2000.  
PA (SAAT/) SAATCIOGLU F.  
Query Match 31.4%; Score 431.5; DB 4; Length 205;  
Best Local Similarity 44.2%; Pred. No. 1.8e-25;  
RESULT 1427  
ID ADE78966 standard; protein; 227 AA.  
DE Human protein modification and maintenance molecule (PMM) -4.  
PN WO2003063688-A2.  
PD 07-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 430; DB 7; Length 227;  
Best Local Similarity 39.2%; Pred. No. 2.7e-25;  
RESULT 1428  
ID AAW69388 standard; protein; 205 AA.  
DE Prostate tumour specific gene clone DE13 protein.  
PN WO9837418-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1429  
ID AAW71872 standard; protein; 205 AA.  
DE Protein encoded by prostate tumour clone P703 splice variant DE13.  
PN WO9837093-A2.  
PD 27-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 2; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1430  
ID AAY82005 standard; protein; 205 AA.  
DE Human immunogenic prostate tumour protein sequence SEQ ID NO:176.  
PN WO200004149-A2.  
PD 27-JAN-2000.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1431  
ID ABG94414 standard; protein; 205 AA.  
DE Human prostate tumour protein partial variant sequence #2.  
PN US2002090372-A1.  
PD 11-JUL-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
Query Match 31.0%; Score 426.5; DB 3; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1432  
ID AAM01120 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200151633-A2.  
PD 19-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1433  
ID AAU69766 standard; protein; 205 AA.  
DE Human prostate cDNA encoded protein #6.  
PN WO200173032-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 31.0%; Score 426.5; DB 4; Length 205;  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1434  
ID AAB74803 standard; protein; 205 AA.  
DE Prostate tumour antigen predicted amino acid sequence for P703P-DE13.

PN WO200125272-A2.  
PD 12-APR-2001.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 4; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1435  
ID AAG99005 standard; protein; 205 AA.  
DE Human prostate-specific amino acid sequence P703P-DE13.  
PN WO200134802-A2.  
PD 17-MAY-2001.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 4; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1436  
ID ABU71656 standard; protein; 205 AA.  
DE Prostate cancer specific antigen P703P #2.  
PN US2002192763-A1.  
PD 19-DEC-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A.  
PA (HURA/) HURAL J.  
PA (MCNE/) MCNEILL P D.  
PA (HOUG/) HOUGHTON R L.  
PA (DBAS/) Y DE BASSOLS C V.  
PA (FOYT/) FOY T M.  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
Length 205;  
RESULT 1437  
ID AAU04964 standard; protein; 205 AA.  
DE Human prostate tumour protein DE13.  
PN US6262245-B1.  
PD 17-JUL-2001.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 4; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1438  
ID ABB95225 standard; protein; 205 AA.  
DE Human P703P-DE13 protein SEQ ID NO 176.  
PN US2002022248-A1.  
PD 21-FEB-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C.  
PA (MITC/) MITCHAM J L.  
PA (HARL/) HARLOCKER S L.  
PA (JIAN/) JIANG Y.  
PA (KALO/) KALOS M D.  
PA (FANG/) FANGER G R.  
PA (RETT/) RETTER M W.  
PA (STOL/) STOLK J A.  
PA (DAYC/) DAY C H.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (LISX/) LI S X.  
PA (WANG/) WANG A.  
PA (SKEI/) SKEIKY Y A W.  
PA (HEPL/) HEPLER W T.  
PA (HEND/) HENDERSON R A. 31.0%; Score 426.5; DB 5; Length 205;  
Query Match

Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1439  
ID ABG76668 standard; protein; 205 AA.  
DE Prostate tumour protein #6.  
PN US2002081580-A1.  
PD 27-JUN-2002.  
PA (XUJJ/) XU J.  
PA (DILL/) DILLON D C. 31.0%; Score 426.5; DB 5; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1440  
ID ABR54337 standard; protein; 205 AA.  
DE Prostate tumour specific protein sequence SEQ ID 176.  
PN WO200289747-A2.  
PD 14-NOV-2002.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 6; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1441  
ID ADB13626 standard; protein; 205 AA.  
DE Human prostate specific protein P703P-DE13.  
PN US2003185830-A1.  
PD 02-OCT-2003.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 7; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1442  
ID ADG26042 standard; protein; 205 AA.  
DE Human prostate-specific polypeptide #6.  
PN US2003157089-A1.  
PD 21-AUG-2003.  
PA (CORI-) CORIXA CORP. 31.0%; Score 426.5; DB 7; Length 205;  
Query Match  
Best Local Similarity 43.7%; Pred. No. 4.5e-25;  
RESULT 1443  
ID ABB09589 standard; protein; 234 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match  
Best Local Similarity 36.4%; Pred. No. 1e-24;  
Length 234;  
RESULT 1444  
ID ADK36957 standard; protein; 281 AA.  
DE Novel human polypeptide SeqID9039.  
PN WO200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC. 30.7%; Score 422.5; DB 5; Length 281;  
Query Match  
Best Local Similarity 39.3%; Pred. No. 1.3e-24;  
RESULT 1445  
ID ABU92024 standard; protein; 218 AA.  
DE Human protein modification and maintenance molecule-4 (PMM-4).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC. 30.7%; Score 422; DB 6; Length 218;  
Query Match  
Best Local Similarity 37.8%; Pred. No. 1.1e-24;  
RESULT 1446  
ID AAB31579 standard; peptide; 225 AA.  
DE Amino acid sequence of cod trypsin isozymes.  
PN WO200078332-A2.  
PD 28-DEC-2000.  
PA (BJAR/) BJARNASON J B. 30.6%; Score 421; DB 4; Length 225;  
Query Match  
Best Local Similarity 44.3%; Pred. No. 1.3e-24;  
RESULT 1447  
ID ADE15982 standard; protein; 218 AA.  
DE G-coupled protein receptor related polypeptide, SEQ ID No 12.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP. 30.6%; Score 420; DB 7; Length 218;  
Query Match

Best Local Similarity 37.8%; Pred. No. 1.5e-24;  
RESULT 1448  
ID ADL93921 standard; protein; 218 AA.  
DE Human G-coupled protein receptor-related protein #6.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL/) LI L.  
PA (GERL/) GERLACH V.  
PA (LIUX/) LIU X.  
PA (MILL/) MILLER C E.  
PA (SPYT/) SPYTEK K A.  
PA (ZERRH/) ZERHUSEN B D.  
PA (PENNA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (ZHON/) ZHONG H.  
PA (SMIT/) SMITHSON G.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (VOSS/) VOSS E Z.  
PA (VERN/) VERNET C A.  
PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (MALY/) MALYANKAR U M.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
Query Match 30.6%; Score 420; DB 8; Length 218;  
Best Local Similarity 37.8%; Pred. No. 1.5e-24;  
RESULT 1449  
ID AAY28641 standard; protein; 207 AA.  
DE Human secreted protein from cDNA clone HKAET41.  
PN WO9940183-A1.  
PD 12-AUG-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 30.4%; Score 418; DB 2; Length 207;  
Best Local Similarity 46.1%; Pred. No. 2e-24;  
RESULT 1450  
ID AAW46773 standard; protein; 233 AA.  
DE Amino acid sequence of Salmonase.  
PN EP814164-A2.  
PD 29-DEC-1997.  
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.  
Query Match 30.4%; Score 417.5; DB 2; Length 233;  
Best Local Similarity 36.6%; Pred. No. 2.5e-24;  
RESULT 1451  
ID AAE21442 standard; protein; 226 AA.  
DE Human trypsin domain consensus protein #2.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 30.3%; Score 416.5; DB 5; Length 226;  
Best Local Similarity 42.6%; Pred. No. 2.9e-24;  
RESULT 1452  
ID ABG75786 standard; protein; 226 AA.  
DE Trypsin domain consensus sequence, SMART.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Query Match 30.3%; Score 416.5; DB 6; Length 226;  
Best Local Similarity 42.6%; Pred. No. 2.9e-24;  
RESULT 1453  
ID ADA05736 standard; protein; 198 AA.  
DE Human NOV18c protein SEQ ID NO:96.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.

Query Match 30.0%; Score 412.5; DB 6; Length 198;  
Best Local Similarity 36.8%; Pred. No. 5.2e-24;  
RESULT 1454  
ID ADN62900 standard; protein; 198 AA.  
DE Human NOV18c.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERRH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENNA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 30.0%; Score 412.5; DB 8; Length 198;  
Best Local Similarity 36.8%; Pred. No. 5.2e-24;  
RESULT 1455  
ID ADA50560 standard; protein; 194 AA.  
DE Prostate specific antigen (PSA/KLK3), SEQ ID NO:15.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ) CENTOCOR INC.  
Query Match 29.8%; Score 409; DB 6; Length 194;  
Best Local Similarity 38.7%; Pred. No. 9.5e-24;  
RESULT 1456  
ID ADG75684 standard; protein; 215 AA.  
DE Human protein modification and maintenance molecule polypeptide SeqID8.  
PN WO2003083084-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 29.8%; Score 409; DB 7; Length 215;  
Best Local Similarity 37.1%; Pred. No. 1.1e-23;  
RESULT 1457  
ID ABM82829 standard; protein; 215 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3078.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.8%; Score 409; DB 8; Length 215;  
Best Local Similarity 37.1%; Pred. No. 1.1e-23;  
RESULT 1458  
ID ABM83248 standard; protein; 299 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3497.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.

Query Match 29.8%; Score 409; DB 8; Length 299;  
Best Local Similarity 38.6%; Pred. No. 1.5e-23;  
RESULT 1459  
ID ADA05738 standard; protein; 181 AA.  
DE Human NOV18d protein SEQ ID NO:98.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 29.7%; Score 408.5; DB 6; Length 181;  
Best Local Similarity 37.4%; Pred. No. 9.6e-24;  
RESULT 1460  
ID ADN62902 standard; protein; 181 AA.  
DE Human NOV18d.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJJ/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERH/) ZERHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIWW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIPI/) DIPIPO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match 29.7%; Score 408.5; DB 8; Length 181;  
Best Local Similarity 37.4%; Pred. No. 9.6e-24;  
RESULT 1461  
ID ABM82641 standard; protein; 222 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2890.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.6%; Score 407; DB 8; Length 222;  
Best Local Similarity 36.7%; Pred. No. 1.6e-23;  
RESULT 1462  
ID AAB08510 standard; protein; 230 AA.  
DE A recombinant protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI ) INSTRUMENTATION LAB.  
Query Match 29.6%; Score 406.5; DB 3; Length 230;  
Best Local Similarity 36.2%; Pred. No. 1.8e-23;  
RESULT 1463  
ID AAW76538 standard; protein; 231 AA.  
DE A. contortrix protein C activator protein fragment.  
PN WO9842850-A1.  
PD 01-OCT-1998.  
PA (RPMS-) RPMS TECHNOLOGY LTD.

Query Match 29.6%; Score 406.5; DB 2; Length 231;  
Best Local Similarity 36.2%; Pred. No. 1.8e-23;  
RESULT 1464  
ID ABB09590 standard; protein; 218 AA.  
DE Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).  
PN CN1181421-A.  
PD 13-MAY-1998.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 29.5%; Score 405.5; DB 5; Length 218;  
Best Local Similarity 36.5%; Pred. No. 2e-23;  
RESULT 1465  
ID ABM84665 standard; protein; 220 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4914.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 29.5%; Score 405; DB 8; Length 220;  
Best Local Similarity 36.7%; Pred. No. 2.2e-23;  
RESULT 1466  
ID AAB08511 standard; protein; 230 AA.  
DE Biosynthetic variant of protein C activator polypeptide.  
PN WO200050612-A2.  
PD 31-AUG-2000.  
PA (INLI ) INSTRUMENTATION LAB.  
Query Match 29.4%; Score 403.5; DB 3; Length 230;  
Best Local Similarity 37.0%; Pred. No. 3e-23;  
RESULT 1467  
ID AAR20557 standard; protein; 234 AA.  
DE Fibrinogenolytic protein #4 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (BADI ) BASF AG.  
Query Match 29.3%; Score 403; DB 2; Length 234;  
Best Local Similarity 36.7%; Pred. No. 3.3e-23;  
RESULT 1468  
ID AAP81333 standard; protein; 255 AA.  
DE Batroxobin.  
PN JP63049084-A.  
PD 01-MAR-1988.  
PA (YAMA/) YAMASHINA I.  
Query Match 29.3%; Score 402; DB 1; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1469  
ID AAR05436 standard; protein; 255 AA.  
DE Batroxobin gene product.  
PN JP02124092-A.  
PD 11-MAY-1990.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 29.3%; Score 402; DB 2; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1470  
ID AAY17869 standard; protein; 255 AA.  
DE Araraca batroxobin.  
PN WO9929838-A1.  
PD 17-JUN-1999.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 29.3%; Score 402; DB 2; Length 255;  
Best Local Similarity 32.9%; Pred. No. 4.3e-23;  
RESULT 1471  
ID AAE21441 standard; protein; 249 AA.  
DE Human trypsin domain consensus protein #1.  
PN WO200226802-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 29.2%; Score 401.5; DB 5; Length 249;  
Best Local Similarity 40.3%; Pred. No. 4.6e-23;  
RESULT 1472  
ID AAM52946 standard; protein; 231 AA.  
DE Batroxobin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 29.1%; Score 400; DB 2; Length 231;



Best Local Similarity 34.2%; Pred. No. 5.6e-23;  
RESULT 1473  
ID AAB11711 standard; protein; 264 AA.  
DE Mouse serine protease BSSP5 (MBSSP5) SEQ ID NO:4.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 28.8%; Score 395.5; DB 3; Length 264;  
Best Local Similarity 39.1%; Pred. No. 1.4e-22;  
RESULT 1474  
ID AAM52945 standard; protein; 236 AA.  
DE Flaboboxin, a snake venom protease.  
PN KR98002267-A.  
PD 30-MAR-1998.  
PA (MOKA-) MOKAM BIOTECHNOLOGY RES INST.  
Query Match 28.7%; Score 394; DB 2; Length 236;  
Best Local Similarity 36.8%; Pred. No. 1.7e-22;  
RESULT 1475  
ID AAR20556 standard; protein; 236 AA.  
DE Fibrinogenolytic protein #3 from snake venom.  
PN DE4023699-A.  
PD 30-JAN-1992.  
PA (IBADI ) BASF AG.  
Query Match 28.6%; Score 393; DB 2; Length 236;  
Best Local Similarity 37.3%; Pred. No. 2e-22;  
RESULT 1476  
ID ABM82831 standard; protein; 233 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3080.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.5%; Score 392; DB 8; Length 233;  
Best Local Similarity 36.8%; Pred. No. 2.3e-22;  
RESULT 1477  
ID AAE39993 standard; protein; 253 AA.  
DE Human adipisin protein #2.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.5%; Score 391; DB 7; Length 253;  
Best Local Similarity 38.0%; Pred. No. 3e-22;  
RESULT 1478  
ID ABG75785 standard; protein; 227 AA.  
DE Trypsin domain consensus sequence, PFAM.  
PN US2002165152-A1.  
PD 07-NOV-2002.  
PA (KAPE/) KAPPELLER-LIBERMANN R.  
Query Match 28.3%; Score 389; DB 6; Length 227;  
Best Local Similarity 40.4%; Pred. No. 3.9e-22;  
RESULT 1479  
ID ADE58223 standard; protein; 253 AA.  
DE Human Protein P00746, SEQ ID NO 4094.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 28.3%; Score 389; DB 7; Length 253;  
Best Local Similarity 38.5%; Pred. No. 4.3e-22;  
RESULT 1480  
ID AAP70758 standard; protein; 269 AA.  
DE Pig pancreas elastase-2.  
PN JP62000276-A.  
PD 06-JAN-1987.  
PA (SANY ) SANKYO CO LTD.  
Query Match 28.2%; Score 388; DB 1; Length 269;  
Best Local Similarity 38.5%; Pred. No. 5.5e-22;  
RESULT 1481  
ID AAE39992 standard; protein; 253 AA.  
DE Human adipisin protein #1.  
PN US2003092620-A1.  
PD 15-MAY-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.2%; Score 387; DB 7; Length 253;

Best Local Similarity 38.5%; Pred. No. 6.2e-22;  
RESULT 1482  
ID AAB11710 standard; protein; 264 AA.  
DE Human serine protease BSSP5 (HBSSP5) SEQ ID NO:2.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 28.1%; Score 386.5; DB 3; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1483  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSET polypeptide clone name vCTRL-1.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GEST ) GENSET SA.  
Query Match 28.1%; Score 386.5; DB 6; Length 264;  
Best Local Similarity 36.8%; Pred. No. 7e-22;  
RESULT 1484  
ID ABU09382 standard; protein; 271 AA.  
DE Consensus sequence of trypsin-like domain.  
PN WO2003031463-A2.  
PD 17-APR-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 28.1%; Score 386; DB 6; Length 271;  
Best Local Similarity 39.1%; Pred. No. 7.9e-22;  
RESULT 1485  
ID ABM82830 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3079.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1486  
ID ABM82644 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:2893.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 28.1%; Score 385.5; DB 8; Length 212;  
Best Local Similarity 36.3%; Pred. No. 6.7e-22;  
RESULT 1487  
ID ABM81778 standard; protein; 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 28.1%; Score 385.5; DB 8; Length 264;  
Best Local Similarity 36.8%; Pred. No. 8.4e-22;  
RESULT 1488  
ID ADR66037 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;  
RESULT 1489  
ID ADR66935 standard; protein; 213 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 233 #4.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 28.0%; Score 385; DB 8; Length 213;  
Best Local Similarity 40.2%; Pred. No. 7.4e-22;

RESULT 1490  
ID AAP61724 standard; protein; 269 AA.  
DE Porcine elastase II.  
PN JP61192289-A.  
PD 26-AUG-1986.  
PA (KIRI ) KIRIN BREWERY KK.  
Query Match 27.9%; Score 384; DB 1; Length 269;  
Best Local Similarity 38.4%; Pred. No. 1.1e-21;  
RESULT 1491  
ID AAR07513 standard; protein; 258 AA.  
DE Ancrod-like polypeptide #2.  
PN EP395375-A.  
PD 31-OCT-1990.  
PA (GLAX ) GLAXO INC.  
PA (KNOL ) KNOLL AG.  
Query Match 27.9%; Score 383; DB 2; Length 258;  
Best Local Similarity 34.3%; Pred. No. 1.3e-21;  
RESULT 1492  
ID AAR05775 standard; protein; 272 AA.  
DE Snake venom ancrod polypeptide.  
PN WO9006362-A.  
PD 14-JUN-1990.  
PA (BADI ) BASF AG.  
PA (BACH/) BACH A.  
Query Match 27.9%; Score 383; DB 2; Length 272;  
Best Local Similarity 33.9%; Pred. No. 1.4e-21;  
RESULT 1493  
ID AAU79393 standard; protein; 171 AA.  
DE Novel human kallikrein KLK15, splice variant #3.  
PN WO200214485-A2.  
PD 21-FEB-2002.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 5; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1494  
ID ADN10933 standard; protein; 171 AA.  
DE Human kallikrein 15, marker of endocrine cancer.  
PN WO2004029285-A2.  
PD 08-APR-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Query Match 27.8%; Score 382.5; DB 8; Length 171;  
Best Local Similarity 35.8%; Pred. No. 9.2e-22;  
RESULT 1495  
ID ABM82642 standard; protein; 212 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2891.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 27.8%; Score 382; DB 8; Length 212;  
Best Local Similarity 35.5%; Pred. No. 1.2e-21;  
RESULT 1496  
ID AAR05772 standard; protein; 250 AA.  
DE Human adipsin gene product from the clone phg31.  
PN WO9006365-A.  
PD 14-JUN-1990.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
PA (DANA-) DANA-FARBER CANCER INST.  
PA (META-) METABOLIC BIOSYSTEMS INC.  
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 37.2%; Pred. No. 1.5e-21;  
RESULT 1497  
ID AAR05421 standard; protein; 250 AA.  
DE Human adipsin/D encoded by a cDNA.  
PN WO9001540-A.  
PD 22-FEB-1990.  
PA (CALB-) CALIF BIOTECHN INC.  
Query Match 27.8%; Score 382; DB 2; Length 250;  
Best Local Similarity 38.4%; Pred. No. 1.5e-21;  
RESULT 1498  
ID ADE58221 standard; protein; 263 AA.  
DE Rat Protein AAB31922, SEQ ID NO 4092.  
PN WO2003016475-A2.

PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 27.7%; Score 381; DB 7; Length 263;  
Best Local Similarity 37.6%; Pred. No. 1.9e-21;  
RESULT 1499  
ID ADN99596 standard; protein; 187 AA.  
DE Novel human protein sequence #412.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 27.6%; Score 379.5; DB 8; Length 187;  
Best Local Similarity 42.7%; Pred. No. 1.7e-21;  
RESULT 1500  
ID ABU92049 standard; protein; 220 AA.  
DE Human protein modification and maintenance molecule-29 (PMMM-29).  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 27.6%; Score 379; DB 6; Length 220;  
Best Local Similarity 37.2%; Pred. No. 2.2e-21;

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OM protein - protein search, using sw model

Run on: March 5, 2005, 17:54:57 ; Search time 174 Seconds  
(without alignments)  
729.860 Million cell updates/sec

Title: US-10-006-856A-194  
Perfect score: 1374  
Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVYTYICKYVDWIRMNRNN 248

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_treml:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1374	100.0	248	1	KLKC_HUMAN
2	952.5	69.3	234	2	Q9CV76
3	630.5	45.9	260	1	KLK8_HUMAN
4	627.5	45.7	260	2	Q8IW69
5	622.5	45.3	260	1	NRPN_MOUSE
6	621.5	45.2	260	1	NRPN_RAT
7	618.5	45.0	250	1	KLKB_HUMAN
8	611	44.5	255	2	Q7JIG6
9	610	44.4	250	2	Q63ZF2
10	608	44.3	254	2	Q8CGR4
11	601	43.7	275	2	Q8IXD7
12	599	43.6	255	2	Q6ISI0
13	599	43.6	256	1	KLKF_HUMAN
14	597.5	43.5	249	2	Q9QYN4
15	597.5	43.5	276	2	Q9QYN3
16	595	43.3	255	2	Q96RQ0
17	588.5	42.8	293	2	Q9D140
18	588	42.8	276	2	Q8CGR6
19	586	42.6	250	2	Q8CGR5
20	578	42.1	242	2	Q80VS4
21	576	41.9	246	2	Q6P3Z0
22	569.5	41.4	248	1	TRY3_CHICK
23	569.5	41.4	251	1	KLKE_HUMAN
24	569.5	41.4	251	2	Q6B089
25	568.5	41.4	250	1	KLK9_HUMAN
26	567	41.3	277	1	KLKD_HUMAN
27	566	41.2	248	1	TRY2_CHICK
28	565	41.1	248	1	TRY1_CHICK
29	564.5	41.1	293	1	KLK5_HUMAN
30	564	41.0	276	1	KLKA_HUMAN
31	563	41.0	244	1	TRY2_XENLA
					P70059 xenopus lae

105	503	36.6	263	1	KLKR_PRANA	P32824	praomys nat
106	502	36.5	249	2	Q9W6K0	Q9w6k0	notothenia
107	502	36.5	259	1	KLKC_RAT	P36376	rattus norv
108	501.5	36.5	237	2	Q915I5	Q91515	fugu rubrip
109	501	36.5	242	2	Q93266	Q93266	pseudopleur
110	501	36.5	247	1	TRY2_HUMAN	P07478	homo sapien
111	501	36.5	247	2	Q9W7Q5	Q9w7q5	paralichthy
112	499.5	36.4	241	1	TRYX_GADMO	Q91041	gadus morhu
113	499	36.3	239	2	Q8N1C9	Q8n1c9	homo sapien
114	498	36.2	249	2	Q788V0	Q788v0	dissostichu
115	498	36.2	254	1	KLK4_HUMAN	Q9y5k2	homo sapien
116	497	36.2	257	2	Q6IE61	Q6ie61	rattus norv
117	497	36.2	258	1	KLK1_PAPHA	Q28773	papio hamad
118	497	36.2	261	2	Q7Z5F4	Q7z5f4	homo sapien
119	496.5	36.1	261	1	KLK5_MOUSE	P15945	mus musculu
120	496	36.1	242	2	Q92099	Q92099	paranotothe
121	496	36.1	247	2	O42158	O42158	petromyzon
122	496	36.1	247	2	O42608	O42608	petromyzon
123	496	36.1	262	2	Q86U61	Q86u61	homo sapien
124	495.5	36.1	257	1	KLK1_MACFA	Q07276	macaca fasc
125	495.5	36.1	261	1	KLKB_MOUSE	P15946	mus musculu
126	495	36.0	261	2	Q7Z5F3	Q7z5f3	homo sapien
127	495	36.0	261	2	Q6H322	Q6h322	equus cabal
128	494.5	36.0	247	1	TRY1_HUMAN	P07477	homo sapien
129	493.5	35.9	248	2	Q66L05	Q66l05	xenopus lae
130	493	35.9	262	1	KLK1_HUMAN	P06870	homo sapien
131	492	35.8	262	2	Q66US9	Q66us9	homo sapien
132	491.5	35.8	241	1	TRY1_GADMO	P16049	gadus morhu
133	491	35.7	256	1	KLK4_MOUSE	P00757	mus musculu
134	490.5	35.7	229	1	TRYP_SQUAC	P00764	squalus aca
135	490.5	35.7	261	1	KLKD_MOUSE	P36368	mus musculu
136	489.5	35.6	261	1	KLKL_MOUSE	Q61759	mus musculu
137	489	35.6	244	1	KLKA_RAT	P36375	rattus norv
138	488	35.5	247	2	Q8NHM4	Q8nhm4	homo sapien
139	487.5	35.5	251	2	Q9DBQ8	Q9dbq8	mus musculu
140	486	35.4	242	2	Q6RI79	Q6ri79	tautogolabr
141	485.5	35.3	234	2	Q9R048	Q9r048	mus musculu
142	485.5	35.3	261	2	O88309	O88309	mus musculu
143	484.5	35.3	251	2	Q8N2U3	Q8n2u3	homo sapien
144	484.5	35.3	259	1	KLKM_MOUSE	P15948	mus musculu
145	484.5	35.3	304	1	TRY3_HUMAN	P35030	homo sapien
146	484	35.2	255	2	Q9Z0M1	Q9z0m1	mus musculu
147	483.5	35.2	261	1	KLK1_RAT	P00758	rattus norv
148	483.5	35.2	265	2	Q68GI7	Q68gi7	rattus norv
149	482	35.1	255	2	Q9JIS2	Q9jis2	mus musculu
150	481.5	35.0	261	1	KLK9_MOUSE	P15949	mus musculu
151	481	35.0	254	2	Q9XSN6	Q9xsn6	sus scrofa
152	480.5	35.0	263	1	KLKR_MOUSE	Q9jmw1	mus musculu
153	479	34.9	261	1	KLK3_MACMU	P33619	macaca mula
154	479	34.9	261	2	Q6DT45	Q6dt45	macaca fasc
155	478.5	34.8	248	2	Q6GPX7	Q6gpx7	xenopus lae
156	478.5	34.8	250	2	Q93265	Q93265	pseudopleur
157	477.5	34.8	256	2	Q6IEI2	Q6iel2	rattus norv
158	477.5	34.8	261	1	KLK1_MOUSE	P00755	mus musculu
159	477.5	34.8	263	1	KLKO_MOUSE	Q61754	mus musculu
160	477	34.7	247	2	Q66PG9	Q66pg9	fugu rubrip
161	476.5	34.7	344	2	Q9W6J9	Q9w6j9	dissostichu
162	476.5	34.7	675	2	Q9W6J8	Q9w6j8	dissostichu
163	475.5	34.6	219	2	Q91036	Q91036	gadus morhu
164	472.5	34.4	235	2	Q66PG8	Q66pg8	fugu rubrip
165	471	34.3	249	2	Q6DIW2	Q6diw2	xenopus tro
166	470.5	34.2	257	2	Q6LDS3	Q6lds3	homo sapien
167	470.5	34.2	261	1	KLK3_HUMAN	P07288	homo sapien
168	470	34.2	258	2	Q71QI1	Q71qi1	trimeresuru
169	469.5	34.2	261	1	KLK8_MOUSE	P07628	mus musculu
170	469.5	34.2	261	2	Q8C232	Q8c232	mus musculu
171	468	34.1	259	1	KLK2_RAT	P00759	rattus norv
172	467.5	34.0	261	1	KLKQ_MOUSE	P36369	mus musculu
173	467	34.0	258	2	Q71QH6	Q71qh6	trimeresuru
174	462.5	33.7	261	2	Q8K0C6	Q8k0c6	mus musculu
175	461.5	33.6	259	1	KLK9_RAT	P07647	rattus norv
176	461	33.6	258	2	Q8AY80	Q8ay80	trimeresuru
177	458.5	33.4	250	1	TRYP_PLEPL	P35034	pleuronecte

178	458.5	33.4	261	1	KLK2_HUMAN	P20151	homo sapien
179	452	32.9	260	2	Q71QJ4	Q71qj4	trimeresuru
180	451	32.8	260	2	Q7T229	Q7t229	bothrops ja
181	450	32.8	260	2	Q8UVX1	Q8uvx1	agkistrodon
182	449	32.7	258	1	VSP1_TRIST	Q91516	trimeresuru
183	448	32.6	258	2	Q8AY78	Q8ay78	trimeresuru
184	446.5	32.5	257	2	Q71QI5	Q71qi5	trimeresuru
185	445.5	32.4	257	1	VSP3_TRIMU	Q91509	trimeresuru
186	444.5	32.4	249	2	Q8JFQ7	Q8jfq7	gadus morhu
187	443	32.2	258	1	VSP2_AGKAC	Q9i8x1	agkistrodon
188	443	32.2	258	1	VSP3_BOTJA	Q9ptu8	bothrops ja
189	439.5	32.0	257	1	VSP7_TRIMU	Q9dg84	trimeresuru
190	439	32.0	279	2	Q9YGU8	Q9ygy8	agkistrodon
191	438	31.9	259	1	VSP1_VIPLE	Q9pt41	vipera lebe
192	437.5	31.8	257	1	VSP2_TRIMU	Q91508	trimeresuru
193	437.5	31.8	257	1	VSP4_TRIMU	Q91510	trimeresuru
194	436.5	31.8	233	2	Q9PT51	Q9pt51	agkistrodon
195	436.5	31.8	255	2	Q03955	Q03955	praomys nat
196	436.5	31.8	257	1	VSP1_TRIMU	Q91507	trimeresuru
197	436.5	31.8	257	1	VSP5_TRIMU	Q91511	trimeresuru
198	435.5	31.7	257	2	Q71QI7	Q71qi7	trimeresuru
199	435	31.7	258	1	VSP2_TRIJE	Q9df67	trimeresuru
200	434	31.6	258	1	VSP3_TRIJE	Q9df66	trimeresuru
201	434	31.6	260	1	VSPB_TRIGA	O13061	trimeresuru
202	434	31.6	260	2	Q71QI9	Q71qi9	trimeresuru
203	433.5	31.6	257	2	Q71QJ0	Q71qj0	trimeresuru
204	433	31.5	260	1	VSP1_AGKHP	Q9ygy2	agkistrodon
205	432	31.4	236	1	VSPA_DABRU	P18964	daboia russ
206	432	31.4	257	2	Q9PTL3	Q9ptl3	agkistrodon
207	432	31.4	260	1	VSP2_AGKHP	Q9ygi6	agkistrodon
208	432	31.4	260	2	Q73800	Q73800	agkistrodon
209	431.5	31.4	205	2	Q96JE0	Q96je0	homo sapien
210	431.5	31.4	257	2	Q71QJ1	Q71qj1	trimeresuru
211	431.5	31.4	261	1	KLK2_HORSE	Q6h321	equus cabal
212	431.5	31.4	261	1	KLKG_MOUSE	P04071	mus musculu
213	431	31.4	260	1	VSPA_TRIGA	O13060	trimeresuru
214	431	31.4	260	2	Q8AY81	Q8ay81	trimeresuru
215	431	31.4	262	1	VSP1_AGKCA	Q91053	agkistrodon
216	429.5	31.3	205	2	Q96JE2	Q96je2	homo sapien
217	429	31.2	176	2	Q8K5D7	Q8k5d7	mus musculu
218	429	31.2	258	1	VSP3_TRIGA	O13063	trimeresuru
219	429	31.2	260	2	Q71QI0	Q71qi0	trimeresuru
220	428.5	31.2	262	2	Q8QHK3	Q8ghk3	crotalus at
221	427	31.1	260	2	Q93502	Q93502	agkistrodon
222	426.5	31.0	257	1	VSPC_TRIGA	O13062	trimeresuru
223	425	30.9	260	1	VSP1_AGKAC	Q9i8x2	agkistrodon
224	424.5	30.9	257	2	Q71QJ3	Q71qj3	trimeresuru
225	423	30.8	204	2	Q96JEL	Q96jel	homo sapien
226	423	30.8	238	1	VSP1_AGKHA	P81176	agkistrodon
227	422.5	30.7	234	2	Q9YGS1	Q9ygs1	agkistrodon
228	422.5	30.7	259	2	Q8UUK2	Q8uuk2	crotalus ad
229	422	30.7	256	2	Q7SVF1	Q7syf1	cerastes ce
230	421.5	30.7	163	2	Q66H01	Q66h01	xenopus lae
231	420.5	30.6	257	2	Q71QI8	Q71qi8	trimeresuru
232	419.5	30.5	234	2	Q8UUJ1	Q8uuji	agkistrodon
233	419	30.5	258	2	Q8QHK2	Q8qhk2	crotalus at
234	418.5	30.5	257	2	Q71QI6	Q71qi6	trimeresuru
235	418	30.4	260	2	Q8AY82	Q8ay82	trimeresuru
236	417	30.3	236	1	VSPG_DABRU	P18965	daboia russ
237	415.5	30.2	178	2	Q93594	Q93594	dicentrarch
238	415.5	30.2	257	2	Q71QH8	Q71qh8	trimeresuru
239	414	30.1	237	2	Q8UUJ2	Q8uuji	agkistrodon
240	413	30.1	258	1	VSP1_TRIGA	O13059	trimeresuru
241	413	30.1	258	2	Q7SZE1	Q7sze1	gloydius sa
242	413	30.1	260	1	VSP1_TRIFL	P05620	trimeresuru
243	411.5	29.9	228	1	VSPA_LACMU	P33589	lacheis mu
244	411	29.9	239	2	Q6T5L0	Q6t5l0	gloydius sh
245	411	29.9	258	2	Q71QH7	Q71qh7	trimeresuru
246	411	29.9	260	2	Q7SZC3	Q7szc3	gallus gall
247	409	29.8	260	1	VSP2_VIPLE	Q9pt40	vipera lebe
248	408.5	29.7	257	2	Q8JH62	Q8jh62	vipera lebe
249	408	29.7	235	1	VSP2_AGKBI	Q9psn3	agkistrodon
250	407	29.6	237	2	Q93421	Q93421	agkistrodon



251	407	29.6	258	1	VSP2_AGKCA	O42207	agkistrodon
252	407	29.6	258	2	Q8AY79	Q8ay79	trimeresuru
253	407	29.6	260	2	VSP2_TRIFL	Q13057	trimeresuru
254	406.5	29.6	231	1	VSP1_AGKCO	P09872	agkistrodon
255	406.5	29.6	257	2	Q71QH5	Q71qh5	trimeresuru
256	405.5	29.5	257	2	Q71QI3	Q71qi3	trimeresuru
257	405	29.5	234	2	Q7SZE2	Q7sze2	agkistrodon
258	403.5	29.4	233	2	Q6IWF1	Q6iwf1	bothrops al
259	402.5	29.3	232	1	VSP1_BOTJA	P81824	bothrops ja
260	402.5	29.3	257	2	Q9YGGJ9	Q9yggj9	agkistrodon
261	402	29.3	255	1	VSPA_BOTAT	P04971	bothrops at
262	402	29.3	260	1	VSP1_TRIJE	Q9df68	trimeresuru
263	402	29.3	260	1	VSP6_TRIMU	Q9dg83	trimeresuru
264	400	29.1	234	1	VSP2_AGKCO	P82981	agkistrodon
265	400	29.1	258	2	Q802F0	Q802f0	agkistrodon
266	399.5	29.1	257	2	Q8QG86	Q8qg86	bothrops in
267	399	29.0	260	2	Q71QJ2	Q71qj2	trimeresuru
268	397	28.9	235	2	Q90Z47	Q90z47	agkistrodon
269	397	28.9	260	2	Q71QI4	Q71qi4	trimeresuru
270	395.5	28.8	264	2	Q9ER05	Q9er05	mus musculus
271	395	28.7	260	2	Q71QH9	Q71qh9	trimeresuru
272	394.5	28.7	257	1	VSP2_BOTJA	O13069	bothrops ja
273	393.5	28.6	264	2	Q9D7P8	Q9d7p8	mus musculus
274	393	28.6	260	1	VSP4_AGKAC	Q9i8w9	agkistrodon
275	392	28.5	258	2	Q71QI2	Q71qi2	trimeresuru
276	391.5	28.5	264	2	Q9EQZ8	Q9eqz8	rattus norv
277	391	28.5	253	2	Q8WZB4	Q8wzb4	homo sapien
278	389	28.3	253	1	CFAD_HUMAN	P00746	homo sapien
279	389	28.3	258	2	Q8JH85	Q8jh85	vipera lebe
280	388.5	28.3	257	1	VSP3_TRIFL	O13058	trimeresuru
281	388	28.2	269	1	EL2_PIG	P08419	sus scrofa
282	387	28.2	181	2	Q8NFV7	Q8nfv7	homo sapien
283	387	28.2	243	2	Q86VJ5	Q86vj5	homo sapien
284	387	28.2	258	2	Q98TT5	Q98tt5	agkistrodon
285	386.5	28.1	257	1	VSP3_AGKAC	Q9i8x0	agkistrodon
286	386	28.1	232	1	VSPA_BOTJA	P81661	bothrops ja
287	386	28.1	258	2	Q9I961	Q9i961	agkistrodon
288	386	28.1	258	2	Q9W7S1	Q9w7s1	agkistrodon
289	386	28.1	260	2	Q6T6S7	Q6t6s7	bitis gabon
290	385.5	28.1	188	1	KLK3_RAT	P15950	rattus norv
291	385.5	28.1	264	1	CTRL_HUMAN	P40313	homo sapien
292	385.5	28.1	264	2	Q9D960	Q9d960	mus musculus
293	385.5	28.1	269	2	Q8IUW0	Q8iuw0	homo sapien
294	384.5	28.0	195	2	Q07277	Q07277	homo sapien
295	382.5	27.8	1524	2	Q91674	Q91674	xenopus lae
296	381	27.7	263	1	CFAD_RAT	P32038	rattus norv
297	380.5	27.7	235	2	Q8N4E0	Q8n4e0	homo sapien
298	380	27.7	157	2	Q6B338	Q6b338	symphysodon
299	380	27.7	455	2	Q7SY86	Q7sy86	xenopus lae
300	379	27.6	220	2	Q8NCW4	Q8ncw4	homo sapien
301	378	27.5	261	2	Q6DHD9	Q6dhd9	brachydanio
302	374.5	27.3	259	1	CFAD_MOUSE	P03953	mus musculus
303	372.5	27.1	228	2	Q6FHW3	Q6fhw3	homo sapien
304	372.5	27.1	261	2	Q8CJF4	Q8cjf4	rattus norv
305	371	27.0	271	1	EL2_RAT	P00774	rattus norv
306	370.5	27.0	204	2	Q86VI7	Q86vi7	homo sapien
307	370.5	27.0	259	1	CFAD_PIG	P51779	sus scrofa
308	370.5	27.0	263	1	CTR2_CANFA	P04813	canis famil
309	370	26.9	234	1	VSP1_AGKRH	P26324	agkistrodon
310	370	26.9	270	2	Q8I9P2	Q8i9p2	aplysina fi
311	369	26.9	330	2	Q6NVR7	Q6nvr7	xenopus tro
312	368.5	26.8	343	1	PSS8_HUMAN	Q16651	homo sapien
313	368	26.8	256	1	TRP3_PSEAM	Q93267	pseudopleur
314	368	26.8	418	1	HATT_HUMAN	O60235	homo sapien
315	367.5	26.7	638	1	KAL_HUMAN	P03952	homo sapien
316	366	26.6	258	1	VSP2_AGKRH	P47797	agkistrodon
317	366	26.6	260	2	Q9W7Q3	Q9w7q3	paralichthy
318	365.5	26.6	245	2	Q9XY60	Q9xy60	ctenocephal
319	365	26.6	263	2	Q7SX97	Q7sx97	brachydanio
320	363.5	26.5	339	2	Q99L44	Q99l44	mus musculus
321	363	26.4	340	2	Q8BJV6	Q8bjv6	mus musculus
322	362.5	26.4	246	1	MCT1_MERUN	P50340	meriones un
323	362.5	26.4	387	2	Q9XY57	Q9xy57	ctenocephal

324	361.5	26.3	267	2	Q7SZ51	Q7sz51	brachydanio
325	361	26.3	255	2	Q6WGR1	Q6wgr1	ictalurus p
326	361	26.3	267	2	Q640B1	Q640e1	xenopus lae
327	359.5	26.2	259	2	Q6AZC2	Q6azc2	brachydanio
328	359.5	26.2	269	2	Q6ISU5	Q6isu5	homo sapien
329	359.5	26.2	277	1	TRY2_ANOGA	P35036	anopheles g
330	359.5	26.2	342	1	PSS8_MOUSE	Q9esd1	mus musculus
331	359	26.1	265	2	Q6P3Z6	Q6p3z6	xenopus tro
332	359	26.1	311	2	Q80XZ3	Q80xz3	rattus norv
333	359	26.1	430	2	Q804X0	Q804x0	fugu rubrip
334	358.5	26.1	245	1	MCT1_SHEEP	P80931	ovis aries
335	358.5	26.1	444	1	FA7_RABIT	P98139	oryctolagus
336	358	26.1	812	1	PLMN_BOVIN	P06868	bos taurus
337	357.5	26.0	232	2	Q9XY45	Q9xy45	ctenocephal
338	357.5	26.0	371	2	Q8MS52	Q8ms52	drosophila
339	357.5	26.0	643	2	Q97506	Q97506	sus scrofa
340	357	26.0	262	1	GRAA_HUMAN	P12544	homo sapien
341	357	26.0	263	1	CTRB_HUMAN	P17538	homo sapien
342	357	26.0	271	1	CTRI_PENVA	Q00871	penaeus van
343	357	26.0	806	1	PLMN_MACEU	O18783	macropus eu
344	357	26.0	1019	1	LFC_TACTR	P28175	tachypleus
345	357	26.0	1019	2	Q8T9S1	Q8t9s1	tachypleus
346	356.5	25.9	261	2	Q9W7Q4	Q9w7q4	paralichthy
347	356.5	25.9	321	1	TRYG_HUMAN	Q9nr2	homo sapien
348	356.5	25.9	321	2	Q96RZ8	Q96rz8	homo sapien
349	355.5	25.9	260	2	Q9V7G4	Q9v7g4	drosophila
350	355.5	25.9	276	1	MCT6_MOUSE	P21845	mus musculus
351	355	25.8	342	1	PSS8_RAT	Q9es87	rattus norv
352	354.5	25.8	249	2	Q6QX59	Q6qx59	lepeophthei
353	354.5	25.8	311	2	Q8WZM5	Q8wzm5	trichoderma
354	354.5	25.8	331	2	Q8RJA6	Q8rja6	mus musculus
355	354.5	25.8	331	2	Q80X17	Q80x17	mus musculus
356	354	25.8	260	2	Q9W7P9	Q9w7p9	paralichthy
357	354	25.8	271	1	EL2_MOUSE	P05208	mus musculus
358	353.5	25.7	263	1	CTRA_GADMO	P47796	gadus morhu
359	353.5	25.7	270	1	TRYT_MERUN	P50342	meriones un
360	353.5	25.7	333	2	Q7Q5Z6	Q7q5z6	anopheles g
361	353	25.7	274	1	MCT6_RAT	P50343	rattus norv
362	353	25.7	314	1	TEST_HUMAN	Q9y6m0	homo sapien
363	353	25.7	456	1	PRTC_CANFA	Q28278	canis famil
364	353	25.7	459	1	PRTC_PIG	Q9glp2	sus scrofa
365	352.5	25.7	263	2	Q6PGS4	Q6pgs4	xenopus lae
366	352.5	25.7	321	2	Q6GNK3	Q6gnk3	xenopus lae
367	352	25.6	111	2	Q9UKR2	Q9ukr2	homo sapien
368	352	25.6	260	1	GRAA_MOUSE	P11032	mus musculus
369	352	25.6	277	2	Q7T0T6	Q7t0t6	xenopus lae
370	352	25.6	304	1	DISP_RAT	P83748	rattus norv
371	352	25.6	505	2	Q966V4	Q966v4	halocynthia
372	351.5	25.6	460	1	PRTC_MOUSE	P33587	mus musculus
373	351	25.5	310	1	DISP_MOUSE	Q9qyz9	mus musculus
374	351	25.5	456	1	PRTC_BOVIN	P00745	bos taurus
375	350.5	25.5	265	2	Q804G1	Q804g1	brachydanio
376	350.5	25.5	274	2	O16133	O16133	anopheles s
377	350.5	25.5	274	2	Q17086	Q17086	anopheles s
378	350.5	25.5	434	2	Q7T3B6	Q7t3b6	brachydanio
379	350	25.5	263	2	Q6GPI1	Q6gpi1	homo sapien
380	350	25.5	268	2	Q6GQE9	Q6gqe9	xenopus lae
381	350	25.5	268	2	Q642S8	Q642s8	xenopus tro
382	350	25.5	271	2	O18487	O18487	penaeus van
383	349.5	25.4	261	2	Q66HW9	Q66hw9	brachydanio
384	349.5	25.4	269	1	EL2A_HUMAN	P08217	homo sapien
385	349.5	25.4	269	2	Q6ICV2	Q6icv2	homo sapien
386	349.5	25.4	277	2	Q96899	Q96899	scolopendra
387	349.5	25.4	371	2	Q8CJ16	Q8cj16	rattus norv
388	349.5	25.4	445	2	Q8CJ17	Q8cj17	rattus norv
389	349.5	25.4	558	2	Q6L711	Q6l711	rattus norv
390	349.5	25.4	1130	2	Q7QIM7	Q7qim7	anopheles g
391	349	25.4	1019	1	LFC_CARRO	Q26422	carcinoscor
392	349	25.4	1083	2	Q26423	Q26423	carcinoscor
393	348.5	25.4	429	2	Q8AVB0	Q8avb0	brachydanio
394	348.5	25.4	503	2	Q8AYE4	Q8aye4	brachydanio
395	348.5	25.4	799	2	Q6PF94	Q6pf94	mus musculus
396	348.5	25.4	811	1	TMS6_MOUSE	Q9dbi0	mus musculus

397	348.5	25.4	818	2	Q6PBA6	Q6pba6 brachydanio	470	339.5	24.7	258	1	GRAM_RAT	Q03238 rattus norv
398	348	25.3	267	1	TRY7_ANOGA	P35041 anopheles g	471	339.5	24.7	271	2	Q803Z4	Q803z4 brachydanio
399	348	25.3	269	2	Q6ISN8	Q6isn8 homo sapien	472	339.5	24.7	333	1	PLMN_CANFA	P80009 canis famil
400	348	25.3	278	2	Q7PNF6	Q7pnf6 anopheles g	473	339	24.7	321	2	Q6IEG0	Q6ie60 rattus norv
401	347.5	25.3	344	2	Q640F8	Q640f8 xenopus lae	474	339	24.7	335	2	Q8VIF2	Q8vif2 mus musculu
402	347	25.3	275	2	Q6FHB8	Q6fhb8 homo sapien	475	339	24.7	458	1	PRTC_RABIT	Q28661 oryctolagus
403	347	25.3	461	1	PRTC_HUMAN	P04070 homo sapien	476	339	24.7	461	1	FA9_HUMAN	P00740 homo sapien
404	346.5	25.2	267	2	Q9BK47	Q9bk47 luidia foli	477	339	24.7	461	1	FA9_PANTR	Q95nd7 pan troglod
405	346.5	25.2	269	2	EL2_BOVIN	O46507 papio hamad	478	339	24.7	625	1	FALL_HUMAN	P03951 homo sapien
406	346.5	25.2	334	2	O46507	Q8i6k0 holotrichia	479	339	24.7	812	1	PLMN_RAT	Q01177 rattus norv
407	346.5	25.2	351	2	Q8I6K0	Q8vca5 mus musculu	480	338.5	24.6	256	2	O18599	O18599 drosophila
408	346.5	25.2	435	1	TMS4_MOUSE	Q9nfy2 anopheles g	481	338.5	24.6	258	1	EL1_HUMAN	Q9uni1 homo sapien
409	346.5	25.2	446	1	FA7_MOUSE	P70375 mus musculu	482	338.5	24.6	258	2	Q867B0	Q867b0 canis famil
410	346.5	25.2	456	2	Q7QC30	Q7qc30 anopheles g	483	338.5	24.6	264	2	O02569	O02569 culex quinq
411	346.5	25.2	461	1	PRTC_RAT	P1394 rattus norv	484	338.5	24.6	307	2	Q6ZND6	Q6znd6 homo sapien
412	346.5	25.2	461	1	Q68FY8	Q68fy8 rattus norv	485	338.5	24.6	455	2	Q8CDR0	Q8cdr0 mus musculu
413	346.5	25.2	461	2	Q804W7	Q804w7 fugu rubrip	486	338.5	24.6	562	2	Q7PN85	Q7pn85 anopheles g
414	346.5	25.2	612	2	Q804W7	Q9qul7 mus musculu	487	338.5	24.6	704	1	CRAR_MOUSE	P98064 mus musculu
415	346	25.2	311	1	TRYG_MOUSE	Q920s2 mus musculu	488	338.5	24.6	802	2	Q6UXD8	Q6uxd8 homo sapien
416	346	25.2	322	2	Q920S2	Q46506 papio hamad	489	338	24.6	210	2	Q63Z11	Q63zi1 xenopus lae
417	345.5	25.1	454	2	O46506	Q967x8 panulirus a	490	338	24.6	365	2	O97366	O97366 holotrichia
418	345.5	25.1	467	2	Q967X8	P54626 drosophila	491	338	24.6	388	2	O44330	O44330 manduca sex
419	345	25.1	253	1	TRYD_DROER	Q9puf3 bothrops ja	492	338	24.6	418	2	Q7PGU3	Q7pgu3 anopheles g
420	344.5	25.1	117	2	Q9PUF3	Q6pk75 homo sapien	493	338	24.6	625	1	THRB_BOVIN	P00735 bos taurus
421	344.5	25.1	187	2	Q6PK75	Q6b051 homo sapien	494	337.5	24.6	238	1	TRY5_AEDAE	P29787 aedes aegyp
422	344.5	25.1	275	2	Q6B051	Q7z410 homo sapien	495	337.5	24.6	261	2	Q6QX60	Q6qx60 lepeophthei
423	344.5	25.1	855	2	Q7Z410	Q7z411 homo sapien	496	337.5	24.6	264	1	GRAX_HUMAN	P49863 homo sapien
424	344.5	25.1	1059	2	Q7Z411	Q8bz04 mus musculu	497	337.5	24.6	282	2	Q9D4I3	Q9d4i3 mus musculu
425	344	25.0	257	2	Q8BZ04	Q6qx61 lepeophthei	498	337.5	24.6	317	2	Q9DGR3	Q9dgr3 xenopus lae
426	344	25.0	265	2	Q6QX61	Q20231 homo sapien	499	337.5	24.6	328	2	Q80Z40	Q80z40 rattus norv
427	344	25.0	275	1	TRB2_HUMAN	Q6nzy1 homo sapien	500	337.5	24.6	432	2	Q6GNA2	Q6gna2 xenopus lae
428	344	25.0	282	2	Q6NZY1	Q8bz10 mus musculu	501	337.5	24.6	471	2	Q8CFE0	Q8cfe0 mus musculu
429	344	25.0	417	2	Q8BZ10	Q02844 mus musculu	502	337	24.5	247	2	Q17039	Q17039 anopheles g
430	343.5	25.0	266	2	O46644	Q921n4 mus musculu	503	337	24.5	263	2	Q9D8X8	Q9d8x8 mus musculu
431	343.5	25.0	273	1	MCT7_MOUSE	Q9h3s3 homo sapien	504	337	24.5	275	2	Q96RZ6	Q96rz6 homo sapien
432	343.5	25.0	273	2	Q921N4	P15944 canis famil	505	337	24.5	432	2	Q6UX37	Q6ux37 homo sapien
433	343.5	25.0	457	1	TMS5_HUMAN	Q8nf86 homo sapien	506	337	24.5	434	1	UROK_CHICK	P15120 gallus gall
434	343	25.0	275	1	TRYT_CANFA	Q8nf86 homo sapien	507	337	24.5	437	1	TMS4_HUMAN	Q9nrs4 homo sapien
435	343	25.0	284	2	Q8NF86	Q7rty9 homo sapien	508	336.5	24.5	247	1	MCT1_PAPHA	P52195 papio hamad
436	343	25.0	318	2	Q7RTY9	O16126 boltenia vi	509	336.5	24.5	251	1	MCT3_SHEEP	O46683 ovis aries
437	342.5	24.9	248	2	O16126	Q9xy52 ctenocephal	510	336.5	24.5	260	2	Q6P2V9	Q6p2v9 xenopus tro
438	342.5	24.9	248	2	Q9XY52	Q8hyj2 bos taurus	511	336.5	24.5	329	2	O42272	O42272 xenopus lae
439	342.5	24.9	271	2	Q8HYJ2	P27435 rattus norv	512	336.5	24.5	428	2	Q8WPM7	Q8wpm7 oikopleura
440	342.5	24.9	273	1	MCT7_RAT	Q6p6w8 rattus norv	513	336.5	24.5	638	1	KAL_MOUSE	P26262 mus musculu
441	342.5	24.9	273	2	Q6P6W8	Q8jhd0 brachydanio	514	336	24.5	227	2	Q8IXI4	Q8ixi4 homo sapien
442	342.5	24.9	433	2	Q8JHD0	Q90yk1 brachydanio	515	336	24.5	263	2	Q9CR35	Q9cr35 m mus muscu
443	342.5	24.9	433	2	Q90YK1	Q8k0d2 mus musculu	516	336	24.5	263	2	Q9DC86	Q9dc86 mus musculu
444	342.5	24.9	517	2	Q8K0D2	Q91y47 mus musculu	517	336	24.5	273	1	TRYT_SHEEP	Q9xsm2 ovis aries
445	342.5	24.9	624	1	FA11_MOUSE	P00747 homo sapien	518	336	24.5	280	2	Q64ID5	Q64id5 anthonomus
446	342.5	24.9	810	1	PLMN_HUMAN	Q8iu80 homo sapien	519	336	24.5	402	2	Q7QB73	Q7qb73 anopheles g
447	342.5	24.9	811	1	TMS6_HUMAN	Q15661 homo sapien	520	336	24.5	416	1	FA9_BOVIN	P00741 bos taurus
448	342.5	24.9	275	1	TRB1_HUMAN	Q7pqr9 anopheles g	521	336	24.5	485	2	Q7PKK0	Q7pkk0 anopheles g
449	342	24.9	355	2	Q7PQR9	P20918 mus musculu	522	336	24.5	556	2	Q803D5	Q803d5 brachydanio
450	342	24.9	812	1	PLMN_MOUSE	P49864 rattus norv	523	336	24.5	654	2	Q6QNF4	Q6qnf4 canis famil
451	341.5	24.9	258	1	GRAX_RAT	Q9er04 mus musculu	524	336	24.5	790	1	PLMN_PIG	P06867 sus scrofa
452	341.5	24.9	455	1	TMS5_MOUSE	Q9v516 drosophila	525	335.5	24.4	258	2	Q6ISM6	Q6ism6 homo sapien
453	341.5	24.9	573	2	Q9V5I6	Q7rty7 homo sapien	526	335.5	24.4	266	1	EL1_BOVIN	Q28153 bos taurus
454	341.5	24.9	1134	2	Q7RTY7	Q9gln2 bos taurus	527	335.5	24.4	275	1	TRYT_PIG	Q9n2d1 sus scrofa
455	341	24.8	251	2	Q9GLN2	Q63zk0 xenopus lae	528	335.5	24.4	389	2	Q9PVX7	Q9pvx7 xenopus lae
456	341	24.8	263	2	Q63ZK0	Q6ira4 xenopus lae	529	335.5	24.4	558	2	Q86YM4	Q86ym4 homo sapien
457	341	24.8	328	2	Q6IRA4	Q7rty8 homo sapien	530	335	24.4	216	2	Q9UD19	Q9ud19 homo sapien
458	341	24.8	572	2	Q7RTY8	Q6dj90 xenopus tro	531	335	24.4	318	2	Q8MNY6	Q8mny6 nilaparvata
459	341	24.8	719	2	Q6DJ90	P21812 mus musculu	532	335	24.4	433	2	Q804X5	Q804x5 gallus gall
460	340.5	24.8	246	1	MCT4_MOUSE	P35035 anopheles g	533	335	24.4	701	2	Q9JJS9	Q9jjs9 rattus norv
461	340.5	24.8	274	1	TRY1_ANOGA	Q8k3u6 rattus norv	534	335	24.4	703	2	Q8CHN8	Q8chn8 rattus norv
462	340.5	24.8	446	1	FA7_RAT	Q9dat3 mus musculu	535	334.5	24.3	247	2	Q70500	Q70500 rattus norv
463	340.5	24.8	624	2	Q9DAT3	Q9xsm1 ovis aries	536	334.5	24.3	263	1	GRAX_MOUSE	Q35205 mus musculu
464	340	24.7	273	2	Q9XSM1	Q8n171 homo sapien	537	334.5	24.3	275	2	Q7YS62	Q7ys62 equus cabal
465	340	24.7	280	2	Q8N171	Q88781 rattus ratt	538	334.5	24.3	537	2	Q9BYE1	Q9bye1 homo sapien
466	340	24.7	297	2	Q88781	O17489 anopheles g	539	334.5	24.3	581	2	Q9BYE2	Q9bye2 homo sapien
467	340	24.7	360	2	O17489	O08732 mesocricetu	540	334	24.3	234	2	Q15096	Q15096 homo sapien
468	339.5	24.7	247	2	O08732	P54625 drosophila	541	334	24.3	264	2	Q8QGF6	Q8qgf6 xenopus lae
469	339.5	24.7	253	1	TRYB_DROER		542	333.5	24.3	253	2	Q8MKZ1	Q8mkz1 drosophila

543	333.5	24.3	253	2	Q8SXZ4	Q8sxz4 drosophila	616	328.5	23.9	365	2	Q7Q1D1	Q7q1d1 anopheles g
544	333.5	24.3	275	2	Q7PNF7	Q7pnf7 anopheles g	617	328.5	23.9	524	2	Q7SXH8	Q7sxb8 brachydanio
545	333.5	24.3	290	1	PR27_HUMAN	Q9bqr3 homo sapien	618	328.5	23.9	615	2	Q6GNK4	Q6gnk4 xenopus lae
546	333.5	24.3	824	2	Q6ICC2	Q6icc2 homo sapien	619	328.5	23.9	681	2	Q7ZT70	Q7zt70 lampetra ja
547	333	24.2	245	1	CTRA_BOVIN	P00766 bos taurus	620	328.5	23.9	683	2	Q8MRH5	Q8mrh5 drosophila
548	333	24.2	256	2	Q9R0K0	Q9r0k0 mus musculu	621	328.5	23.9	786	1	STUB_DROME	Q05319 drosophila
549	333	24.2	285	1	FA9_CAVPO	P16295 cavia porce	622	328.5	23.9	787	2	Q9VEY6	Q9vey6 drosophila
550	333	24.2	320	2	Q7TOX2	Q7tox2 xenopus lae	623	328	23.9	226	1	COGS_UCAPU	P00771 uca pugilat
551	333	24.2	355	2	Q7PEW0	Q7pew0 anopheles g	624	328	23.9	328	2	Q6BEA2	Q6bea2 rattus norv
552	333	24.2	360	2	Q7PEV7	Q7pev7 anopheles g	625	328	23.9	452	1	FA9_CANFA	P19540 canis famil
553	332.5	24.2	247	2	O35342	O35342 mesocricetu	626	328	23.9	767	2	Q9DGR2	Q9dgr2 xenopus lae
554	332.5	24.2	254	2	Q8T637	Q8t637 aedes aegyp	627	327.5	23.8	247	1	MCT1_MACFA	P56435 macaca fasc
555	332.5	24.2	260	2	Q8T4P6	Q8t4p6 lepeophthei	628	327.5	23.8	263	2	Q9TYI6	Q9tyi6 penaeus van
556	332.5	24.2	262	2	Q8T4P7	Q8t4p7 lepeophthei	629	327.5	23.8	266	2	Q27761	Q27761 penaeus van
557	332.5	24.2	263	2	Q7Z1D5	Q7z1d5 lepeophthei	630	327.5	23.8	269	2	Q96QV5	Q96qv5 homo sapien
558	332.5	24.2	264	2	Q7YSS9	Q7yss9 lepeophthei	631	327.5	23.8	269	2	Q6ISM5	Q6ism5 homo sapien
559	332.5	24.2	490	1	TMS2_MOUSE	Q9jiq8 mus musculu	632	327.5	23.8	269	2	Q6GN82	Q6gn82 xenopus lae
560	332.5	24.2	638	1	KAL_RAT	P14272 rattus norv	633	327	23.8	259	1	DEF3_DERFA	P49275 dermatophag
561	332.5	24.2	810	1	PLMN_ERIEU	Q29485 erinaceus e	634	327	23.8	263	2	Q7SY54	Q7sy54 xenopus lae
562	332.5	24.2	810	1	PLMN_MACMU	P12545 macaca mula	635	327	23.8	270	2	Q27824	Q27824 uca pugilat
563	332	24.2	247	2	Q7OT74	Q7ot74 equus cabal	636	327	23.8	466	2	Q6SA95	Q6sa95 felis silve
564	332	24.2	251	2	Q7Q9W2	Q7q9w2 anopheles g	637	327	23.8	600	2	Q7ZTR2	Q7ztr2 xenopus lae
565	332	24.2	258	2	Q97399	Q97399 phaedon coc	638	326.5	23.8	248	1	GRAC_MOUSE	P08882 mus musculu
566	332	24.2	266	2	Q92077	Q92077 gadus morhu	639	326.5	23.8	263	2	Q6GNF7	Q6gnf7 xenopus lae
567	332	24.2	277	2	Q8SQ44	Q8sq44 sus scrofa	640	326.5	23.8	266	1	EL1_PIG	P00772 sus scrofa
568	332	24.2	355	2	Q9NFU1	Q9nful anopheles g	641	326.5	23.8	266	2	Q91X79	Q91x79 mus musculu
569	331.5	24.1	250	2	Q8T4P4	Q8t4p4 lepeophthei	642	326.5	23.8	369	2	Q7QKL1	Q7qkl1 anopheles g
570	331.5	24.1	254	2	Q8MMK9	Q8mmk9 aedes aegyp	643	326.5	23.8	490	2	Q7TN04	Q7tn04 mus musculu
571	331.5	24.1	256	1	TRYA_DROME	P04814 drosophila	644	326	23.7	248	1	GRZ1_RAT	Q06605 rattus norv
572	331.5	24.1	260	2	Q8T4P5	Q8t4p5 lepeophthei	645	326	23.7	271	1	CTR2_PENVA	P36178 penaeus van
573	331.5	24.1	263	2	Q9PWQ6	Q9pwq6 gadus morhu	646	326	23.7	329	2	Q7PEV8	Q7pev8 anopheles g
574	331.5	24.1	264	2	Q6GPY5	Q6gpy5 xenopus lae	647	326	23.7	432	2	Q7QKL4	Q7qkl4 anopheles g
575	331.5	24.1	275	1	TRY3_ANOGA	P35037 anopheles g	648	325.5	23.7	259	2	Q8IRE0	Q8ire0 drosophila
576	331	24.1	263	1	CTRB_RAT	P07338 rattus norv	649	325.5	23.7	261	1	DER3_DERPT	P39675 dermatophag
577	331	24.1	622	1	THRB_HUMAN	P00734 homo sapien	650	325.5	23.7	268	2	O46151	O46151 pacifastacu
578	331	24.1	622	2	Q7Z7P3	Q7z7p3 homo sapien	651	325.5	23.7	306	1	BSS4_MOUSE	Q9er10 mus musculu
579	331	24.1	722	2	Q8AW90	Q8aw90 lampetra ja	652	325.5	23.7	891	2	Q9VV38	Q9vv38 drosophila
580	331	24.1	722	2	Q9PSZ5	Q9psz5 lampetra ja	653	324.5	23.6	146	2	Q9DDE1	Q9dde1 brachydanio
581	330.5	24.1	247	1	MCT1_HUMAN	P23946 homo sapien	654	324.5	23.6	228	2	Q7Q153	Q7q153 anopheles g
582	330.5	24.1	256	1	TRYA_DROER	P54624 drosophila	655	324.5	23.6	263	2	Q7PUB9	Q7pub9 anopheles g
583	330.5	24.1	269	2	Q6ISP9	Q6isp9 homo sapien	656	324.5	23.6	275	1	TRYA_HUMAN	P15157 homo sapien
584	330.5	24.1	560	2	Q14520	Q14520 homo sapien	657	324.5	23.6	391	2	Q9V3Z2	Q9v3z2 drosophila
585	330.5	24.1	638	2	Q8R0P5	Q8r0p5 mus musculu	658	324	23.6	253	1	TRYB_DROME	P35004 drosophila
586	330	24.0	236	2	Q7SIG3	Q7sig3 salmo salar	659	324	23.6	257	1	GRAM_HUMAN	P51124 homo sapien
587	330	24.0	253	2	Q9V5Y3	Q9v5y3 drosophila	660	324	23.6	266	2	Q9W7Q0	Q9w7q0 paralichthy
588	330	24.0	266	2	Q8I916	Q8i916 blomia trop	661	324	23.6	459	1	FA9_MOUSE	P16294 mus musculu
589	330	24.0	282	1	FA9_RAT	P16296 rattus norv	662	324	23.6	1019	1	ENTK_HUMAN	P98073 homo sapien
590	329.5	24.0	4548	1	APOA_HUMAN	P08519 homo sapien	663	323.5	23.5	277	2	Q80WM7	Q80wm7 mus musculu
591	329.5	24.0	237	2	Q29464	Q29464 bos taurus	664	323.5	23.5	299	2	Q9VS87	Q9vs87 drosophila
592	329.5	24.0	248	2	Q8T4P2	Q8t4p2 lepeophthei	665	323.5	23.5	328	2	Q8BUR6	Q8bjr6 mus musculu
593	329.5	24.0	253	1	TRYD_DROME	P42276 drosophila	666	323.5	23.5	466	1	FA7_HUMAN	P08709 homo sapien
594	329.5	24.0	262	2	Q7Z1D6	Q7z1d6 lepeophthei	667	323.5	23.5	490	2	Q6P7D7	Q6p7d7 rattus norv
595	329.5	24.0	266	2	Q8WR10	Q8wr10 paralithode	668	323.5	23.5	608	2	Q9PTW7	Q9ptw7 struthio ca
596	329.5	24.0	269	1	EL2B_HUMAN	P08218 homo sapien	669	323.5	23.5	875	1	NETR_HUMAN	P56730 homo sapien
597	329.5	24.0	320	2	Q7PEV6	Q7pev6 anopheles g	670	323	23.5	281	2	O46137	O46137 lumbricus r
598	329.5	24.0	578	2	Q6Q0I7	Q6q0i7 bos taurus	671	323	23.5	296	2	Q9VDV1	Q9vdv1 drosophila
599	329.5	23.9	1420	1	APOA_MACMU	P14417 macaca mula	672	323	23.5	540	2	Q800Y7	Q800y7 meleagris g
600	329	23.9	216	1	VSPB_LACMU	P84036 lachesis mu	673	323	23.5	653	1	HGFA_MOUSE	Q9r098 mus musculu
601	329	23.9	264	2	O08643	O08643 mus musculu	674	323	23.5	653	2	Q8VCS4	Q8vcs4 mus musculu
602	329	23.9	279	2	Q99MS4	Q99ms4 mus musculu	675	322.5	23.5	249	2	Q6QX62	Q6qx62 lepeophthei
603	329	23.9	307	2	Q7TML0	Q7tml0 mus musculu	676	322.5	23.5	258	2	Q9W5U8	Q9wsu8 drosophila
604	329	23.9	572	2	Q8BIK6	Q8bik6 mus musculu	677	322.5	23.5	324	1	TEST_MOUSE	Q9jhj7 mus musculu
605	329	23.9	575	2	Q7Q9W3	Q7q9w3 anopheles g	678	322.5	23.5	336	2	Q80YD8	Q80yd8 mus musculu
606	329	23.9	722	2	Q6NUF5	Q6nuf5 xenopus lae	679	322.5	23.5	372	2	Q9YIK6	Q9ylk6 anopheles g
607	328.5	23.9	239	2	Q8T4P3	Q8t4p3 lepeophthei	680	322.5	23.5	581	2	Q9XZM7	Q9xzm7 strongyloce
608	328.5	23.9	245	1	CTRB_GADMO	P80646 gadus morhu	681	322	23.4	210	2	Q68DS2	Q68ds2 homo sapien
609	328.5	23.9	253	1	TRYG_DROME	P42277 drosophila	682	322	23.4	699	1	CRAR_HUMAN	P48740 h complemen
610	328.5	23.9	260	1	MCT1_RAT	P09650 rattus norv	683	322	23.4	1303	2	Q66S84	Q66s84 oikopleura
611	328.5	23.9	261	2	Q8T4P1	Q8t4p1 lepeophthei	684	321.5	23.4	263	2	O62562	O62562 penaeus van
612	328.5	23.9	275	2	Q86TM8	Q86tm8 homo sapien	685	321.5	23.4	265	2	Q7SYX8	Q7syx8 xenopus lae
613	328.5	23.9	276	2	Q86UA5	Q86ua5 homo sapien	686	321.5	23.4	266	2	Q9D936	Q9d936 mus musculu
614	328.5	23.9	338	1	PLMN_HORSE	P80010 equus cabal	687	321.5	23.4	679	2	Q96PQ8	Q96pq8 homo sapien
615	328.5	23.9	364	2	Q9NAS9	Q9nas9 anopheles g	688	321	23.4	226	1	DDN1_BOVIN	P80219 bos taurus



689	321	23.4	230	2	Q6IE13	Q6iel3 rattus norv
690	321	23.4	247	1	MCT2_MERUN	P50341 meriones un
691	321	23.4	248	1	NKP1_RAT	P18291 rattus norv
692	321	23.4	269	1	TRYM_CANFA	P19236 canis famil
693	321	23.4	411	2	Q9VUF0	Q9vuf0 drosophila
694	321	23.4	655	1	HGFA_HUMAN	Q04756 homo sapien
695	320.5	23.3	247	1	GRAB_MOUSE	P04187 mus musculu
696	320.5	23.3	312	2	Q7M755	Q7m755 mus musculu
697	320	23.3	249	2	Q9W7Q1	Q9w7q1 paralichthy
698	320	23.3	489	2	Q7Q432	Q7q432 anopheles g
699	320	23.3	536	2	Q7PX72	Q7px72 anopheles g
700	319.5	23.3	265	2	Q6GNG0	Q6gng0 xenopus lae
701	319.5	23.3	559	2	Q6P7U0	Q6p7u0 mus musculu
702	319.5	23.3	607	2	Q6DFJ5	Q6dfj5 xenopus lae
703	319	23.2	241	2	Q7PFF7	Q7pff7 anopheles g
704	319	23.2	264	2	Q8IPY7	Q8ipy7 drosophila
705	319	23.2	270	2	Q64ID1	Q64id1 anthonomus
706	319	23.2	320	2	Q8CIR7	Q8cir7 rattus norv
707	319	23.2	461	2	Q95ND6	Q95nd6 pan troglod
708	319	23.2	1034	1	ENTK_PIG	P98074 sus scrofa
709	318.5	23.2	343	1	PLMN_SHEEP	P81286 ovis aries
710	318.5	23.2	418	2	Q6IEI5	Q6iel5 rattus norv
711	318.5	23.2	490	2	Q920K3	Q920k3 rattus norv
712	318	23.1	232	2	Q94508	Q94508 dermatophag
713	318	23.1	258	2	Q7YRZ7	Q7yrz7 bos taurus
714	318	23.1	261	2	Q962G7	Q962g7 culex pipie
715	318	23.1	265	2	O18488	O18488 penaeus van
716	318	23.1	271	1	FA9_PIG	P16293 sus scrofa
717	318	23.1	274	1	FA9_SHEEP	P16291 ovis aries
718	318	23.1	295	2	Q69EZ8	Q69ez8 homo sapien
719	318	23.1	618	1	THRB_MOUSE	P19221 mus musculu
720	317.5	23.1	245	1	CTRB_BOVIN	P00767 bos taurus
721	317.5	23.1	246	1	GRAH_HUMAN	P20718 homo sapien
722	317.5	23.1	248	2	Q9XYX9	Q9xyx9 rhyzopertha
723	317.5	23.1	256	1	TRYE_DROER	P54627 drosophila
724	317.5	23.1	374	2	Q9VUG2	Q9vug2 drosophila
725	317.5	23.1	559	1	TPA_MOUSE	P11214 mus musculu
726	317.5	23.1	604	1	CFAI_RAT	Q9wuw3 rattus norv
727	317.5	23.1	617	2	Q8JIS1	Q8jis1 triakis scy
728	317	23.1	248	2	Q63636	Q63636 rattus norv
729	317	23.1	624	2	Q95ME7	Q95me7 oryctolagus
730	316.5	23.0	246	1	MCT1_MOUSE	P11034 mus musculu
731	316.5	23.0	441	2	Q8I9I7	Q8i9i7 manduca sex
732	316.5	23.0	607	2	Q91001	Q91001 gallus gall
733	316	23.0	246	2	Q9XY46	Q9xy46 ctenocephal
734	316	23.0	259	2	Q69EZ7	Q69ez7 homo sapien
735	316	23.0	263	2	O02570	O02570 culex quinq
736	316	23.0	269	2	Q9CQ52	Q9cq52 m mus muscu
737	316	23.0	269	2	Q9D7T9	Q9d7t9 mus musculu
738	315.5	23.0	254	1	TRY3_AEDAE	P29786 aedes aegyp
739	315.5	23.0	264	2	O62561	O62561 penaeus van
740	315.5	23.0	265	2	Q66KR6	Q66kr6 xenopus lae
741	315.5	23.0	266	1	EL1_RAT	P00773 rattus norv
742	315.5	23.0	314	2	Q9VR15	Q9vr15 drosophila
743	315.5	23.0	374	2	Q7QCS5	Q7qcs5 anopheles g
744	315.5	23.0	392	1	EAST_DROME	P13582 drosophila
745	315.5	23.0	453	2	Q812A6	Q812a6 mus musculu
746	315.5	23.0	492	1	FA10_BOVIN	P00743 bos taurus
747	315	22.9	248	2	Q63224	Q63224 rattus norv
748	315	22.9	280	2	Q66NX6	Q66nx6 canis famil
749	315	22.9	323	2	Q96QG4	Q96qg4 homo sapien
750	315	22.9	617	1	THRB_RAT	P18292 rattus norv
751	315	22.9	686	1	MAS2_HUMAN	O00187 homo sapien
752	314.5	22.9	256	1	TRYE_DROME	P35005 drosophila
753	314.5	22.9	261	2	Q6IDF4	Q6idf4 drosophila
754	314.5	22.9	283	2	Q6UWY2	Q6uwy2 homo sapien
755	314.5	22.9	453	1	TMS3_MOUSE	Q8klt0 mus musculu
756	314.5	22.9	609	2	Q7M761	Q7m761 mus musculu
757	314.5	22.9	680	2	Q868H7	Q868h7 branchiosto
758	314	22.9	275	1	TRY4_ANOGA	P35038 anopheles g
759	314	22.9	280	2	Q7Q494	Q7q494 anopheles g
760	314	22.9	280	2	Q66NX5	Q66nx5 canis famil
761	314	22.9	422	2	Q8WVC1	Q8wvc1 homo sapien

762	314	22.9	629	2	Q6AZS7	Q6azs7 xenopus lae
763	314	22.9	855	1	ST14_HUMAN	Q9y5y6 homo sapien
764	313.5	22.8	261	1	EUM3_EURMA	O97370 euroglyphus
765	313.5	22.8	321	2	Q80Y38	Q80y38 mus musculu
766	313.5	22.8	326	2	Q9D9M0	Q9d9m0 mus musculu
767	313.5	22.8	364	2	Q9I7V4	Q9i7v4 drosophila
768	313.5	22.8	425	2	Q804X7	Q804x7 gallus gall
769	313	22.8	241	2	Q9I7L2	Q9i7l2 drosophila
770	313	22.8	336	2	Q8CIR9	Q8cir9 mus musculu
771	313	22.8	420	2	Q90504	Q90504 eptatretus
772	313	22.8	613	2	Q03711	Q03711 xenopus lae
773	313	22.8	697	2	Q8CG43	Q8cg43 rattus norv
774	313	22.8	733	2	Q920S0	Q920s0 mus musculu
775	313	22.8	733	2	Q8CD27	Q8cd27 mus musculu
776	313	22.8	855	2	Q9JJI7	Q9jji7 rattus norv
777	312.5	22.7	241	2	Q8IYP2	Q8iyp2 homo sapien
778	312.5	22.7	271	2	Q8T9R6	Q8t9r6 culex pipie
779	312.5	22.7	274	1	TRY5_ANOGA	P35039 anopheles g
780	312.5	22.7	300	2	Q96EF3	Q96ef3 homo sapien
781	312.5	22.7	390	2	Q9Y157	Q9y157 drosophila
782	312.5	22.7	615	1	FA12_HUMAN	P00748 homo sapien
783	312.5	22.7	680	2	Q868H5	Q868h5 branchiosto
784	312.5	22.7	1234	2	Q7PIQ7	Q7piq7 anopheles g
785	312.5	22.7	1322	2	Q7PNR7	Q7pnr7 anopheles g
786	312.5	22.7	1322	2	Q9NJS5	Q9njs5 anopheles g
787	312	22.7	295	2	Q8CIP7	Q8cip7 rattus norv
788	312	22.7	374	2	Q8I862	Q8i862 dermatacitor
789	312	22.7	597	2	O35727	O35727 mus musculu
790	312	22.7	597	2	Q6PER0	Q6per0 mus musculu
791	312	22.7	609	2	Q80YC5	Q80yc5 mus musculu
792	311.5	22.7	255	2	Q25227	Q25227 lucilia cup
793	311.5	22.7	255	2	Q7TNI0	Q7tni0 mus musculu
794	311.5	22.7	293	2	Q23528	Q23528 caenorhabdi
795	311.5	22.7	566	1	TPA_BOVIN	Q28198 bos taurus
796	311.5	22.7	645	2	Q7PWE4	Q7pwe4 anopheles g
797	311.5	22.7	761	1	NETR_MOUSE	O08762 mus musculu
798	311.5	22.7	1322	2	Q9NAT0	Q9nat0 anopheles g
799	311	22.6	249	2	Q6IE11	Q6iel1 rattus norv
800	311	22.6	250	2	Q9V514	Q9v514 drosophila
801	311	22.6	261	1	CATG_MOUSE	P28293 mus musculu
802	311	22.6	431	1	ACRO_RABIT	P48038 oryctolagus
803	311	22.6	433	1	UROK_BOVIN	Q05589 bos taurus
804	311	22.6	1035	1	ENTK_BOVIN	P98072 bos taurus
805	311	22.6	1042	1	CORI_HUMAN	Q9y5q5 homo sapien
806	310.5	22.6	247	1	MCT2_RAT	P00770 rattus norv
807	310.5	22.6	259	2	Q7PFI7	Q7pfi7 anopheles g
808	310.5	22.6	371	2	Q8MRY3	Q8mry3 drosophila
809	310.5	22.6	473	2	Q7PV63	Q7pv63 anopheles g
810	310.5	22.6	559	1	TPA_RAT	P19637 rattus norv
811	310.5	22.6	1374	2	Q9V5U0	Q9vsu0 drosophila
812	310.5	22.6	1449	2	Q9ULI2	Q9uli2 drosophila
813	310.5	22.6	1450	2	Q8IQB8	Q8iqb8 drosophila
814	310.5	22.6	1462	2	Q9ULI3	Q9uli3 drosophila
815	310.5	22.6	2382	2	Q9BI19	Q9bi19 drosophila
816	310.5	22.6	2409	2	Q960G6	Q960g6 drosophila
817	310.5	22.6	2786	2	Q9VSU2	Q9vsu2 drosophila
818	310	22.6	275	1	FA9_RABIT	P16292 oryctolagus
819	310	22.6	327	2	Q7Q530	Q7q530 anopheles g
820	310	22.6	483	2	Q8T8X4	Q8t8x4 drosophila
821	310	22.6	483	2	Q9VK10	Q9vk10 drosophila
822	310	22.6	1111	2	Q80YN4	Q80yn4 rattus norv
823	309.5	22.5	246	2	Q9EPR0	Q9epr0 mus musculu
824	309.5	22.5	255	2	Q9Y7A9	Q9y7a9 metarhizium
825	309.5	22.5	265	2	Q9VVT3	Q9vvt3 drosophila
826	309.5	22.5	284	2	Q7Q493	Q7q493 anopheles g
827	309.5	22.5	482	1	FA10_RAT	Q63207 rattus norv
828	309.5	22.5	868	2	Q9Y1V3	Q9y1v3 polyandroca
829	309	22.5	285	2	Q8CG42	Q8cg42 rattus norv
830	309	22.5	404	2	Q7QKL2	Q7qkl2 anopheles g
831	308.5	22.5	240	2	Q6IE06	Q6ie06 rattus norv
832	308.5	22.5	246	1	MCT9_MOUSE	O35164 mus musculu
833	308.5	22.5	260	2	Q6VPU6	Q6vpu6 sarcoptes s
834	308	22.4	125	2	Q804G0	Q804g0 spherooides



835	308	22.4	300	2	Q8I9P4	Q8i9p4 aurelia aur	908	302	22.0	269	2	Q7PW17	Q7pw17 anopheles g
836	308	22.4	317	1	BSS4 HUMAN	Q9gzn4 homo sapien	909	302	22.0	321	2	Q6MZL2	Q6mz12 homo sapien
837	308	22.4	334	2	Q6UXEO	Q6uxe0 homo sapien	910	302	22.0	394	1	URTG_DESRO	P49150 desmodus ro
838	308	22.4	335	2	Q86PB3	Q86pb3 drosophila	911	302	22.0	477	1	URT2_DESRO	P15638 desmodus ro
839	308	22.4	377	2	Q9VB68	Q9vb68 drosophila	912	301.5	21.9	241	2	Q8BW11	Q8bw11 m mus muscu
840	308	22.4	408	2	Q8MR95	Q8mr95 drosophila	913	301.5	21.9	394	2	P91817	P91817 tachypleus
841	308	22.4	698	2	Q6GPF9	Q6gpf9 xenopus lae	914	301.5	21.9	505	2	Q7QCV2	Q7qcv2 anopheles g
842	307.5	22.4	255	2	Q7PFI6	Q7pf16 anopheles g	915	301	21.9	255	1	CATG HUMAN	P08311 homo sapien
843	307.5	22.4	471	2	Q804X6	Q804x6 gallus gall	916	301	21.9	255	2	O34289	O34289 salvelinus
844	307.5	22.4	676	2	Q6DUJ6	Q6duj6 cyprinus ca	917	301	21.9	268	2	Q17030	Q17030 anopheles g
845	307	22.3	135	2	Q62284	Q62284 mus musculu	918	301	21.9	279	2	Q7PX39	Q7px39 anopheles g
846	307	22.3	250	2	Q17036	Q17036 anopheles g	919	301	21.9	279	2	Q7TNX3	Q7tnx3 mus musculu
847	307	22.3	259	1	CTR1 ANOGA	Q27289 anopheles g	920	301	21.9	283	2	Q95V22	Q95v22 lumbricus b
848	307	22.3	318	2	Q7Q9W4	Q7q9w4 anopheles g	921	301	21.9	417	2	Q8VHK8	Q8vkh8 mus musculu
849	307	22.3	417	1	HEPS HUMAN	P05981 homo sapien	922	301	21.9	417	2	Q8VDV1	Q8vdv1 mus musculu
850	307	22.3	726	2	Q7QBF4	Q7qbp4 anopheles g	923	301	21.9	431	1	URTB_DESRO	P98121 desmodus ro
851	306.5	22.3	308	2	Q9W454	Q9w454 drosophila	924	301	21.9	728	2	Q96RS4	Q96rs4 homo sapien
852	306.5	22.3	365	2	Q7QGL1	Q7qgl1 anopheles g	925	300.5	21.9	239	2	Q7T2H1	Q7t2h1 xenopus lae
853	306.5	22.3	375	1	PCE TACTR	P21902 tachypleus	926	300.5	21.9	276	2	P91894	P91894 arenicola m
854	306.5	22.3	418	2	Q8SZK2	Q8szk2 drosophila	927	300.5	21.9	278	2	Q68FN6	Q68fn6 brachydanio
855	306.5	22.3	468	2	Q9UUG3	Q9u0g3 pacifastacu	928	300.5	21.9	386	2	Q8I924	Q8i924 bombyx mori
856	306	22.3	162	2	Q6UBW2	Q6ubw2 homo sapien	929	300.5	21.9	424	2	Q9VA88	Q9va88 drosophila
857	306	22.3	247	2	Q8N1D2	Q8nld2 homo sapien	930	300.5	21.9	433	2	Q8MHY7	Q8mhy7 oryctolagus
858	306	22.3	266	2	Q6AZC0	Q6azc0 brachydanio	931	300.5	21.9	433	2	Q8MIL0	Q8mil0 oryctolagus
859	306	22.3	362	2	Q9W453	Q9w453 drosophila	932	300.5	21.9	442	1	UROK_PIG	P04185 sus scrofa
860	306	22.3	685	2	Q91WP0	Q91wp0 mus musculu	933	300.5	21.9	562	2	Q8SQ23	Q8sq23 sus scrofa
861	305.5	22.2	228	2	Q9XY49	Q9xy49 ctenocephal	934	300	21.8	245	1	GILX_HELHO	P43685 heloderma h
862	305.5	22.2	246	2	Q91VB1	Q91vb1 mus musculu	935	300	21.8	270	2	Q8WR11	Q8wr11 paralithode
863	305.5	22.2	256	1	HYP4 HYPLI	P35587 hypoderma l	936	300	21.8	291	2	Q8IQ89	Q8iq89 drosophila
864	305.5	22.2	274	2	Q6GNF0	Q6gnf0 xenopus lae	937	300	21.8	417	2	Q8VHJ4	Q8vhj4 rattus norv
865	305.5	22.2	383	2	Q77102	Q77102 manduca sex	938	300	21.8	698	2	Q9PU71	Q9pu71 xenopus lae
866	305.5	22.2	418	2	Q9VA87	Q9va87 drosophila	939	299.5	21.8	241	2	Q63637	Q63637 rattus norv
867	305.5	22.2	441	2	Q804X2	Q804x2 fugu rubrip	940	299.5	21.8	246	1	MCTX_MOUSE	Q00356 mus musculu
868	305	22.2	247	1	GRAB HUMAN	P10144 h granzyme	941	299.5	21.8	254	2	Q6DBS8	Q6db88 brachydanio
869	305	22.2	281	2	Q67BC3	Q67bc3 homo sapien	942	299.5	21.8	254	2	Q19023	O19023 macaca mula
870	305	22.2	307	2	Q64ID2	Q64id2 anthonomus	943	299.5	21.8	258	1	CTR2_ANOGA	Q17025 anopheles g
871	305	22.2	391	2	Q7PXJ5	Q7pxj5 anopheles g	944	299.5	21.8	272	2	Q7Q9W5	Q7q9w5 anopheles g
872	305	22.2	395	2	Q9BZW1	Q9bzw1 homo sapien	945	299.5	21.8	282	2	Q7PT16	Q7pt16 anopheles g
873	305	22.2	532	2	Q7PX73	Q7px73 anopheles g	946	299.5	21.8	325	2	O15944	O15944 sarcophaga
874	304.5	22.2	258	2	Q9XY53	Q9xy53 ctenocephal	947	299.5	21.8	372	2	Q9W2C8	Q9w2c8 drosophila
875	304.5	22.2	271	2	Q7Q820	Q7q820 anopheles g	948	299.5	21.8	430	2	Q6RUJ3	Q6ruj3 trichinella
876	304.5	22.2	384	2	Q9XY63	Q9xy63 ctenocephal	949	299.5	21.8	436	1	ACRO_MOUSE	P23578 mus musculu
877	304.5	22.2	492	1	TMS2 HUMAN	O15393 homo sapien	950	299.5	21.8	465	2	Q9BJL7	Q9bjl7 trichinella
878	304.5	22.2	492	2	Q96T73	Q96t73 homo sapien	951	299.5	21.8	615	2	Q8IZZ5	Q8izz5 homo sapien
879	304	22.1	268	1	CLCR HUMAN	Q99895 homo sapien	952	299.5	21.8	974	2	Q90WD8	Q90wd8 bufo japoni
880	304	22.1	272	2	Q9XYV6	Q9xyv6 rhyzopertha	953	299.5	21.8	1069	1	ENTK_MOUSE	P97435 mus musculu
881	304	22.1	375	2	Q8I7W8	Q8i7w8 dermacentor	954	299	21.8	256	2	Q6V1Q1	Q6v1q1 verticilliu
882	304	22.1	393	2	Q6RX66	Q6rx66 armigeres s	955	299	21.8	437	1	ACRO_RAT	P29293 rattus norv
883	304	22.1	400	2	Q9VCJ8	Q9vcj8 drosophila	956	298.5	21.7	235	2	Q91004	Q91004 gecko gecko
884	304	22.1	423	2	Q8EM10	Q8bml0 mus musculu	957	298.5	21.7	248	2	Q9VQ98	Q9vq98 drosophila
885	304	22.1	543	2	Q9BU99	Q9bu99 homo sapien	958	298.5	21.7	249	1	MCT1_CANFA	P21842 canis famil
886	304	22.1	562	1	TPA HUMAN	P00750 homo sapien	959	298.5	21.7	350	2	Q7QKY0	Q7qky0 anopheles g
887	304	22.1	589	2	Q6RJA5	Q6pja5 homo sapien	960	298.5	21.7	407	1	FA7_BOVIN	P22457 bos taurus
888	304	22.1	685	2	Q9Z338	Q9z338 mus musculu	961	298.5	21.7	433	2	Q8T3A2	Q8t3a2 ciona intes
889	304	22.1	1379	2	Q9V4N6	Q9v4n6 drosophila	962	298.5	21.7	733	2	Q9VTX9	Q9vtx9 drosophila
890	304	22.1	1397	2	Q7KQ09	Q7kqg9 drosophila	963	298	21.7	235	2	Q28731	Q28731 oryctolagus
891	303.5	22.1	240	2	Q7SYQ8	Q7syq8 xenopus lae	964	298	21.7	255	2	O18435	O18435 helicoverta
892	303.5	22.1	244	1	MCT2_MOUSE	P15119 mus musculu	965	298	21.7	268	2	Q8T4T4	Q8t4t4 aedes aegyp
893	303.5	22.1	246	1	MCT4_RAT	P97592 rattus norv	966	298	21.7	348	2	Q86WS5	Q86ws5 homo sapien
894	303.5	22.1	278	2	Q7Q492	Q7q492 anopheles g	967	297.5	21.7	254	2	O76520	O76520 stomoxys ca
895	303.5	22.1	309	2	Q27083	Q27083 tachypleus	968	297.5	21.7	256	2	Q6MJY6	Q6m jy6 bdellovibri
896	303.5	22.1	603	1	CFAI_MOUSE	Q61129 mus musculu	969	297.5	21.7	269	2	Q6AZF9	Q6azf9 xenopus lae
897	303.5	22.1	761	2	Q99JC8	Q99jc8 rattus norv	970	297.5	21.7	277	2	Q8IQ10	Q8iq10 drosophila
898	303	22.1	246	1	MCT2_SHEEP	P79204 ovis aries	971	297.5	21.7	293	2	Q7Q8F9	Q7q8f9 anopheles g
899	303	22.1	259	2	Q6JPG5	Q6jpg5 neodiprion	972	297.5	21.7	408	2	Q9VW19	Q9vw19 drosophila
900	302.5	22.0	119	2	Q9NR68	Q9nr68 homo sapien	973	297.5	21.7	435	1	SNAK_DROME	P05049 drosophila
901	302.5	22.0	223	2	Q9VBY4	Q9vby4 drosophila	974	297.5	21.7	472	2	Q7Q182	Q7qi82 anopheles g
902	302.5	22.0	273	1	TRY6 ANOGA	P35040 anopheles g	975	297.5	21.7	486	2	Q7PX74	Q7px74 anopheles g
903	302.5	22.0	1004	2	P79953	P79953 xenopus lae	976	297.5	21.7	519	2	Q8T3A3	Q8t3a3 ciona intes
904	302.5	22.0	1113	1	CORI_MOUSE	Q9z319 mus musculu	977	297.5	21.7	616	2	O97507	O97507 sus scrofa
905	302	22.0	247	2	Q6T376	Q6t376 eisenia foe	978	297	21.6	237	1	TRYP_ASTFL	P00765 astacus flu
906	302	22.0	255	1	TRY4 IUCCU	P35044 lucilia cup	979	297	21.6	247	1	MCT5_MOUSE	P21844 mus musculu
907	302	22.0	268	2	Q9W7Q2	Q9w7q2 paralichthy	980	297	21.6	256	2	Q9XY51	Q9xy51 ctenocephal

981	297	21.6	268	2	Q9BIG0	Q9big0 aedes aegyp
982	297	21.6	284	2	Q8IRX5	Q8irx5 drosophila
983	297	21.6	352	2	Q6UWB4	Q6uwb4 homo sapien
984	297	21.6	369	2	Q6AXZ6	Q6axz6 rattus norv
985	297	21.6	454	1	TMS3_HUMAN	P57727 homo sapien
986	297	21.6	477	1	URT1_DESRO	P98119 desmodus ro
987	296.5	21.6	248	1	GRAF_MOUSE	P08883 mus musculu
988	296.5	21.6	270	1	EL3B_HUMAN	P08861 homo sapien
989	296.5	21.6	272	2	Q9V5X6	Q9v5x6 drosophila
990	296.5	21.6	273	2	Q7JYN3	Q7jyn3 drosophila
991	296.5	21.6	581	2	Q960I5	Q960i5 drosophila
992	296.5	21.6	1047	2	Q9VZH2	Q9vzh2 drosophila
993	296	21.5	265	2	Q74696	Q74696 phaeosphaer
994	296	21.5	279	2	Q9QZ74	Q9qz74 rattus norv
995	296	21.5	281	2	Q76898	Q76898 drosophila
996	296	21.5	314	2	Q6RUT2	Q6rut2 mus musculu
997	296	21.5	318	2	Q80UR4	Q80ur4 mus musculu
998	295.5	21.5	239	2	Q9GME0	Q9gme0 ornithorhyn
999	295.5	21.5	239	2	Q9I2I8	Q9i2i8 oncorhynchu
1000	295.5	21.5	270	2	Q9VRS4	Q9vrs4 drosophila
1001	295.5	21.5	433	1	UROK_MOUSE	P06869 mus musculu
1002	295.5	21.5	449	2	Q9VDU8	Q9vdu8 drosophila
1003	295.5	21.5	453	2	Q6ZMC3	Q6zmc3 homo sapien
1004	295	21.5	260	2	Q9V6P6	Q9v6p6 drosophila
1005	295	21.5	267	2	Q6DGW4	Q6dgw4 brachydanio
1006	295	21.5	268	2	Q8T4T5	Q8t4t5 aedes aegyp
1007	295	21.5	269	2	Q95KW7	Q95kw7 bos taurus
1008	295	21.5	358	2	Q45029	Q45029 drosophila
1009	295	21.5	553	2	Q6P7I9	Q6p7i9 xenopus lae
1010	294.5	21.4	244	2	Q8I6N3	Q8i6n3 eisenia foe
1011	294.5	21.4	575	2	Q8IRB8	Q8irb8 drosophila
1012	294	21.4	247	2	Q6IE57	Q6ie57 rattus norv
1013	294	21.4	259	2	Q9XY61	Q9xy61 ctenocephal
1014	294	21.4	265	2	Q9VHF8	Q9vhf8 drosophila
1015	294	21.4	271	2	Q9GTK2	Q9gtk2 culex quinq
1016	294	21.4	283	2	Q25394	Q25394 lumbricus r
1017	294	21.4	283	2	Q8ITU7	Q8itu7 lumbricus r
1018	294	21.4	293	2	Q7Z5A4	Q7z5a4 homo sapien
1019	294	21.4	303	2	Q76900	Q76900 drosophila
1020	293.5	21.4	246	2	Q6IE10	Q6iel0 rattus norv
1021	293.5	21.4	256	2	Q9XY11	Q9xyy1 rhyzopertha
1022	293.5	21.4	257	2	Q7Z0G1	Q7z0g1 phlebotomus
1023	293.5	21.4	302	2	Q8SYZ7	Q8syz7 drosophila
1024	293.5	21.4	302	2	Q9W586	Q9w586 drosophila
1025	293.5	21.4	431	1	UROK_HUMAN	P00749 homo sapien
1026	293.5	21.4	845	2	Q6GR54	Q6gr54 xenopus lae
1027	293	21.3	246	2	Q9R2C8	Q9r2c8 rattus norv
1028	293	21.3	247	1	MCT3_RAT	P50339 rattus norv
1029	293	21.3	265	1	SER1_DROME	P17205 drosophila
1030	293	21.3	268	2	Q16900	Q16900 aedes aegyp
1031	293	21.3	268	2	Q8NOR8	Q8n0r8 aedes aegyp
1032	293	21.3	277	2	Q9VFN8	Q9vfn8 drosophila
1033	293	21.3	278	2	Q8MQQ2	Q8mqq2 drosophila
1034	293	21.3	301	2	Q7Q6U2	Q7q6u2 anopheles g
1035	293	21.3	427	2	Q6Y2X4	Q6y2x4 manduca sex
1036	293	21.3	433	1	UROK_PAPCY	P16227 papio cynoc
1037	293	21.3	777	2	Q8CAN9	Q8can9 mus musculu
1038	293	21.3	855	1	ST14_MOUSE	P56677 mus musculu
1039	292.5	21.3	235	2	Q90387	Q90387 cynops pyrr
1040	292.5	21.3	236	2	Q9Z1H1	Q9z1h1 mus musculu
1041	292.5	21.3	390	2	Q8MP08	Q8mp08 bombyx mori
1042	292.5	21.3	469	2	Q9GMD9	Q9gmd9 ornithorhyn
1043	292	21.3	257	2	Q8T639	Q8t639 aedes aegyp
1044	292	21.3	268	1	CLCR_RAT	P55091 rattus norv
1045	292	21.3	270	2	Q8T4A8	Q8t4a8 drosophila
1046	292	21.3	276	2	Q97398	Q97398 phaedon coc
1047	292	21.3	332	2	Q8SY58	Q8sys8 drosophila
1048	292	21.3	413	2	Q8T9T2	Q8t9t2 aedes aegyp
1049	292	21.3	475	2	Q804W9	Q804w9 fugu rubrip
1050	292	21.3	688	2	Q868H6	Q868h6 branchiosto
1051	291.5	21.2	216	1	CTR2_VESOR	P00768 vespa orien
1052	291.5	21.2	238	2	Q9Z1D3	Q9z1d3 rattus norv
1053	291.5	21.2	255	2	Q9NBC9	Q9nbc9 glossina mo

1054	291.5	21.2	270	2	Q7Q5A6	Q7q5a6 anopheles g
1055	291	21.2	239	2	Q6LCU4	Q6lcu4 lumbricus r
1056	291	21.2	271	2	Q542I3	Q542i3 streptomyce
1057	291	21.2	436	1	HEPS_MOUSE	Q35453 mus musculu
1058	291	21.2	678	2	Q9JJ58	Q9jjs8 rattus norv
1059	290.5	21.1	483	2	Q7PKJ7	Q7pkj7 anopheles g
1060	290.5	21.1	681	2	Q7Q554	Q7q554 anopheles g
1061	290	21.1	149	2	Q6DTY8	Q6dty8 hypophthalm
1062	290	21.1	256	1	HYPB_HYPLI	P35588 hypoderma l
1063	290	21.1	257	2	Q27440	Q27440 aedes aegyp
1064	290	21.1	390	2	Q8I927	Q8i927 hyphantria
1065	289.5	21.1	246	2	Q9BLI7	Q9bli7 lumbricus r
1066	289.5	21.1	248	1	GRAG_MOUSE	P13366 mus musculu
1067	289.5	21.1	257	2	Q6R560	Q6r560 ostrinia nu
1068	289.5	21.1	317	2	Q8K4I7	Q8k4i7 mus musculu
1069	289	21.0	260	2	Q7RTY3	Q7rty3 homo sapien
1070	289	21.0	278	2	Q7QHS0	Q7qhs0 anopheles g
1071	289	21.0	339	2	Q9QX91	Q9qx91 rattus norv
1072	289	21.0	366	2	Q9QX85	Q9qx85 rattus norv
1073	289	21.0	376	1	FAI0_TROCA	P81428 tropidechis
1074	289	21.0	441	2	Q9XXV0	Q9xxv0 bombyx mori
1075	289	21.0	541	2	Q9QX90	Q9qx90 rattus norv
1076	289	21.0	583	1	CFAI_HUMAN	P05156 homo sapien
1077	289	21.0	623	2	Q9JJP3	Q9jjp3 rattus norv
1078	289	21.0	643	2	Q9QX84	Q9qx84 rattus norv
1079	288.5	21.0	255	2	Q9XY62	Q9xy62 ctenocephal
1080	288.5	21.0	264	2	Q7Q290	Q7q290 anopheles g
1081	288.5	21.0	315	2	Q8IRR3	Q8irr3 drosophila
1082	288.5	21.0	317	2	Q8K4D1	Q8k4d1 mus musculu
1083	288.5	21.0	438	2	Q6ZWK6	Q6zwk6 homo sapien
1084	288.5	21.0	442	2	Q804X1	Q804x1 fugu rubrip
1085	288.5	21.0	1047	2	Q240I9	Q240i9 drosophila
1086	288	21.0	257	2	Q9NB49	Q9nb49 aedes aegyp
1087	288	21.0	261	2	Q8IRE1	Q8ire1 drosophila
1088	288	21.0	405	2	Q8MZM7	Q8mzm7 anopheles g
1089	288	21.0	405	2	Q7PGY0	Q7pgy0 anopheles g
1090	288	21.0	421	2	Q60491	Q60491 cavia porce
1091	288	21.0	730	2	Q6Q1Q8	Q6qlq8 gallus gall
1092	287.5	20.9	234	2	Q90244	Q90244 acipenser t
1093	287.5	20.9	244	2	Q6T375	Q6t375 eisenia foe
1094	287.5	20.9	249	2	Q7KRD0	Q7krd0 drosophila
1095	287.5	20.9	472	2	Q6IGB2	Q6igb2 drosophila
1096	287.5	20.9	603	1	FAI2_CAVPO	Q04962 cavia porce
1097	287.5	20.9	845	2	Q63ZQ6	Q63zq6 xenopus lae
1098	287	20.9	204	2	Q6S9W8	Q6s9w8 homo sapien
1099	287	20.9	244	2	Q6LAM0	Q6lam0 homo sapien
1100	287	20.9	256	2	Q25081	Q25081 hypoderma l
1101	287	20.9	268	2	Q8T4T3	Q8t4t3 aedes aegyp
1102	287	20.9	273	2	Q9VEM5	Q9vem5 drosophila
1103	287	20.9	416	2	Q86T26	Q86t26 homo sapien
1104	287	20.9	422	1	DES1_HUMAN	Q9ul52 homo sapien
1105	287	20.9	423	2	Q6UW31	Q6uw31 homo sapien
1106	287	20.9	481	1	FAI0_MOUSE	Q88947 mus musculu
1107	287	20.9	581	2	Q8I925	Q8i925 hyphantria
1108	286.5	20.9	218	1	CTR2_VESCR	P00769 vespa crabr
1109	286.5	20.9	220	2	Q7QM61	Q7qm61 anopheles g
1110	286.5	20.9	376	2	Q7PTP7	Q7ptp7 anopheles g
1111	286.5	20.9	425	2	Q7PZ85	Q7pz85 anopheles g
1112	286	20.8	235	2	Q6XGZ4	Q6xgz4 homo sapien
1113	286	20.8	254	1	CTRL_HALRU	P35003 haliotis ru
1114	286	20.8	272	2	Q7Q483	Q7q483 anopheles g
1115	286	20.8	416	2	Q8BZ13	Q8bz13 mus musculu
1116	286	20.8	416	2	Q8BZ30	Q8bz30 mus musculu
1117	286	20.8	443	2	Q8JHC9	Q8jhc9 brachydanio
1118	286	20.8	667	2	Q9BJM1	Q9bjm1 trichinella
1119	285.5	20.8	175	2	Q6PLJ9	Q6plj9 squilla ora
1120	285.5	20.8	248	1	MCT8_RAT	P97594 rattus norv
1121	285.5	20.8	270	1	EL3A_HUMAN	P09093 homo sapien
1122	285.5	20.8	270	2	Q96QL8	Q96ql8 homo sapien
1123	285.5	20.8	270	2	Q91039	Q91039 gadus morhu
1124	285.5	20.8	289	2	Q8MR67	Q8mr67 drosophila
1125	285.5	20.8	290	2	Q9VRT2	Q9vrt2 drosophila
1126	285	20.7	470	2	Q8T3A1	Q8t3a1 ciona intes

1127	284.5	20.7	172	2	Q6T776	Q6t776 homo sapien
1128	284.5	20.7	245	2	Q6DKQ3	Q6dkq3 eisenia foe
1129	284.5	20.7	253	1	CAC3_BOVIN	P05805 bos taurus
1130	284.5	20.7	564	2	Q7RTZ1	Q7rtz1 homo sapien
1131	284	20.7	235	2	Q6B4R4	Q6b4r4 bos taurus
1132	284	20.7	243	2	O01309	O01309 botryllus s
1133	284	20.7	257	2	Q86PL8	Q86pl8 aedes aegypt
1134	283.5	20.6	268	2	Q9XY56	Q9xy56 ctenocephal
1135	283.5	20.6	707	2	Q8QGV0	Q8qgv0 cyprinus ca
1136	283	20.6	247	1	TRYP_SIMVI	P35048 simulum vi
1137	283	20.6	320	2	Q7QKL3	Q7qkl3 anopheles g
1138	283	20.6	382	2	Q76HL1	Q76hl1 mus musculu
1139	282.5	20.6	245	2	Q7PJQ0	Q7pjq0 anopheles g
1140	282.5	20.6	246	2	Q8I7P0	Q8i7p0 lumbricus b
1141	282.5	20.6	267	2	Q9VLF5	Q9vlf5 drosophila
1142	282.5	20.6	269	2	Q9V929	Q9v929 drosophila
1143	282.5	20.6	424	2	Q6R558	Q6r558 ostrinia nu
1144	282.5	20.6	687	2	Q69DK8	Q69dk8 sus scrofa
1145	282	20.5	258	2	Q6JKF3	Q6jkf3 neodiprion
1146	282	20.5	259	2	Q18600	Q18600 drosophila
1147	282	20.5	263	2	Q9NB92	Q9nb92 agrotis ips
1148	282	20.5	416	1	HEPS_RAT	Q05511 rattus norv
1149	282	20.5	686	2	Q6Q1Q9	Q6q1q9 gallus gall
1150	282	20.5	688	2	Q868H4	Q868h4 branchiosto
1151	281.5	20.5	258	2	Q9NGY6	Q9ngy6 aedes aegypt
1152	281.5	20.5	291	2	Q8MLC5	Q8mlc5 drosophila
1153	281.5	20.5	388	2	Q7Z1F0	Q7z1f0 cotesia rub
1154	281.5	20.5	430	2	Q7PNQ4	Q7pnq4 anopheles g
1155	281	20.5	262	2	Q7Z0G5	Q7z0g5 phlebotomus
1156	281	20.5	267	2	Q9VA66	Q9va66 drosophila
1157	281	20.5	329	2	Q7QB72	Q7qb72 anopheles g
1158	281	20.5	564	2	Q8MKB1	Q8mbk1 oryctolagus
1159	280.5	20.4	227	2	Q7PHB4	Q7phb4 anopheles g
1160	280.5	20.4	255	2	Q97100	Q97100 anopheles d
1161	280.5	20.4	270	2	Q7Q0N6	Q7q0n6 anopheles g
1162	280.5	20.4	365	2	Q9Y1K7	Q9y1k7 anopheles g
1163	280.5	20.4	410	2	Q7QJ44	Q7qj44 anopheles g
1164	280.5	20.4	424	2	Q6R559	Q6r559 ostrinia nu
1165	280.5	20.4	439	2	Q8BHM9	Q8bhm9 m mus muscu
1166	280	20.4	241	2	Q7PQB3	Q7pqb3 anopheles g
1167	280	20.4	254	1	TRYP_SARBU	P51588 sarcophaga
1168	280	20.4	267	2	Q8SYK8	Q8syk8 drosophila
1169	280	20.4	271	2	Q9V4W5	Q9v4w5 drosophila
1170	280	20.4	282	2	Q25395	Q25395 lumbricus r
1171	280	20.4	336	2	Q7RTY5	Q7rty5 homo sapien
1172	280	20.4	420	2	Q6IE14	Q6iel4 rattus norv
1173	280	20.4	494	2	Q9VJD7	Q9vjd7 drosophila
1174	279.5	20.3	745	2	Q9PVY3	Q9pvy3 cyprinus ca
1175	279	20.3	242	2	Q6T374	Q6t374 eisenia foe
1176	279	20.3	248	2	Q920S1	Q920s1 mus musculu
1177	279	20.3	267	2	Q9VA67	Q9va67 drosophila
1178	279	20.3	280	1	TRYZ_DROME	P42280 drosophila
1179	279	20.3	280	2	Q9V5X8	Q9v5x8 drosophila
1180	279	20.3	319	2	Q9VRS5	Q9vrs5 drosophila
1181	279	20.3	329	2	Q9GL10	Q9gl10 ovis aries
1182	279	20.3	385	2	Q25101	Q25101 herdmania m
1183	279	20.3	694	2	Q8R099	Q8r099 mus musculu
1184	279	20.3	694	2	Q6P6T1	Q6p6t1 rattus norv
1185	279	20.3	721	2	Q7ZT69	Q7zt69 lampetra ja
1186	278.5	20.3	269	2	Q7PWT2	Q7pwt2 anopheles g
1187	278.5	20.3	326	2	Q7ZZ80	Q7zz80 brachydanio
1188	278.5	20.3	330	2	Q6IE62	Q6ie62 rattus norv
1189	278.5	20.3	593	1	FA12_BOVIN	P98140 bos taurus
1190	278	20.2	239	2	Q9NKC5	Q9nkc5 drosophila
1191	278	20.2	474	2	Q7PZH7	Q7pzh7 anopheles g
1192	278	20.2	490	1	FA10_RABIT	O19045 oryctolagus
1193	278	20.2	501	2	Q7QCVO	Q7qcv0 anopheles g
1194	277.5	20.2	245	2	Q9BLI8	Q9bli8 lumbricus r
1195	277.5	20.2	266	2	Q24091	Q24091 drosophila
1196	277.5	20.2	271	2	Q76519	Q76519 stomoxys ca
1197	277.5	20.2	845	2	Q9DGR1	Q9dgr1 xenopus lae
1198	277	20.2	252	2	Q76498	Q76498 diaprepes a
1199	277	20.2	272	2	Q82KG0	Q82kg0 streptomyce

1200	277	20.2	273	2	Q9VKA8	Q9vka8 drosophila
1201	277	20.2	398	2	Q8MKP4	Q8mkp4 drosophila
1202	277	20.2	1629	2	Q9V513	Q9v513 drosophila
1203	277	20.2	1674	2	Q8SY35	Q8sy35 drosophila
1204	276.5	20.1	257	2	Q97099	Q97099 anopheles d
1205	276.5	20.1	262	2	Q9VSJ2	Q9vsj2 drosophila
1206	276	20.1	254	1	PRN3_MOUSE	Q61096 mus musculu
1207	276	20.1	257	2	Q8I8E4	Q8i8e4 ochlerotatu
1208	276	20.1	271	1	S24D_ANOGA	Q17004 anopheles g
1209	276	20.1	300	2	Q7Q6U1	Q7q6u1 anopheles g
1210	276	20.1	302	2	Q9VCJ0	Q9vcj0 drosophila
1211	276	20.1	376	1	FA10_HOPST	P83370 hoplocephal
1212	276	20.1	488	1	FA10_HUMAN	P00742 homo sapien
1213	276	20.1	717	2	Q8AXR1	Q8axr1 xenopus lae
1214	275.5	20.1	246	2	Q6DKQ2	Q6dkq2 eisenia foe
1215	275.5	20.1	249	2	Q8C1Q8	Q8clq8 mus musculu
1216	275.5	20.1	256	2	Q8I8E5	Q8i8e5 ochlerotatu
1217	275.5	20.1	258	2	Q6NLM5	Q6nlm5 drosophila
1218	275.5	20.1	262	2	Q9V5X9	Q9v5x9 drosophila
1219	275.5	20.1	296	2	Q8T9U6	Q8t9u6 aedes aegypt
1220	275	20.0	237	2	Q17035	Q17035 anopheles g
1221	275	20.0	256	2	Q25082	Q25082 hypoderma l
1222	275	20.0	260	2	Q9VSJ1	Q9vsj1 drosophila
1223	275	20.0	262	2	Q7Z0G3	Q7z0g3 phlebotomus
1224	275	20.0	284	2	Q8AXQ8	Q8axq8 xenopus lae
1225	275	20.0	317	2	Q7Q619	Q7q619 anopheles g
1226	275	20.0	496	2	Q8CHP7	Q8chp7 cavia porce
1227	275	20.0	717	2	Q8AXR0	Q8axr0 xenopus lae
1228	274.5	20.0	695	1	CASP_MESAU	P15156 mesocricetu
1229	274	19.9	87	2	Q9CQ78	Q9cq78 m mus muscu
1230	274	19.9	265	2	Q9VHF7	Q9vhf7 drosophila
1231	273	19.9	125	2	Q86VI8	Q86vi8 homo sapien
1232	273	19.9	247	1	MCT8_MOUSE	P43430 mus musculu
1233	273	19.9	254	2	Q8K597	Q8k597 rattus norv
1234	273	19.9	257	2	Q8I8E3	Q8i8e3 aedes polyn
1235	273	19.9	258	1	TRYU_DROER	P54629 drosophila
1236	273	19.9	265	2	Q17800	Q17800 caenorhabdi
1237	273	19.9	288	2	Q9VEM8	Q9vem8 drosophila
1238	273	19.9	377	2	P79343	P79343 bos taurus
1239	272.5	19.8	258	2	Q9GME1	Q9gme1 ornithorhyn
1240	272.5	19.8	262	1	TRYU_DROME	P42279 drosophila
1241	272.5	19.8	282	2	Q7PX30	Q7px30 anopheles g
1242	272.5	19.8	287	2	Q9VTV2	Q9vtv2 drosophila
1243	272.5	19.8	432	1	UROK_RAT	P29598 rattus norv
1244	272.5	19.8	537	2	Q804W8	Q804w8 fugu rubrip
1245	272.5	19.8	978	2	P91777	P91777 pacifastacu
1246	272	19.8	243	2	O01310	O01310 botryllus s
1247	272	19.8	262	1	TRYT_DROME	P42278 drosophila
1248	272	19.8	262	2	Q9V5Y0	Q9v5y0 drosophila
1249	272	19.8	288	2	Q8SX49	Q8sx49 drosophila
1250	272	19.8	475	1	FA10_CHICK	P25155 gallus gall
1251	272	19.8	492	2	Q7Z155	Q7z155 chiromantes
1252	272	19.8	688	1	C1S_HUMAN	P09871 homo sapien
1253	272	19.8	688	2	Q8CFG8	Q8cfg8 mus musculu
1254	271.5	19.8	250	2	Q7PWE3	Q7pwe3 anopheles g
1255	271.5	19.8	257	2	Q8IS83	Q8is83 aedes albop
1256	271.5	19.8	262	2	Q9NB91	Q9nb91 agrotis ips
1257	271.5	19.8	267	2	Q9V942	Q9v942 drosophila
1258	271.5	19.8	272	2	Q9VRS3	Q9vrs3 drosophila
1259	271.5	19.8	833	2	O96442	O96442 strongyloce
1260	271	19.7	247	2	Q70164	Q70164 mesocricetu
1261	271	19.7	253	2	Q9XY50	Q9xy50 ctenocephal
1262	271	19.7	275	2	Q7Z0B4	Q7z0b4 stomoxys ca
1263	271	19.7	1801	2	Q8WSJ2	Q8wsj2 bombyx mori
1264	270.5	19.7	219	2	Q7PJ75	Q7pj75 anopheles g
1265	270.5	19.7	245	2	Q6IE56	Q6ie56 rattus norv
1266	270.5	19.7	248	1	GRAD_MOUSE	P11033 mus musculu
1267	270.5	19.7	256	1	TRYB_MANSE	P35046 manduca sex
1268	270.5	19.7	420	2	Q7Q235	Q7q235 anopheles g
1269	270	19.7	253	2	O18440	O18440 helicoverpa
1270	270	19.7	297	2	Q7Q6U4	Q7q6u4 anopheles g
1271	270	19.7	694	2	Q70542	Q70542 rattus norv
1272	269.5	19.6	248	1	GRZ2_RAT	Q06606 rattus norv



1273	269.5	19.6	339	2	Q6BDA8	Q6bda8 penaeus jap	1346	262	19.1	266	2	Q9VMX7	Q9vmx7 drosophila
1274	269	19.6	235	2	Q9GTK7	Q9gtk7 aedes albop	1347	262	19.1	272	2	Q8SZG4	Q8szg4 drosophila
1275	269	19.6	244	2	Q8MWR5	Q8mwr5 dermatophag	1348	262	19.1	390	2	Q7PVQ3	Q7pvq3 anopheles g
1276	269	19.6	375	2	Q9NAS8	Q9nas8 anopheles g	1349	262	19.1	427	2	Q7Q6T1	Q7q6t1 anopheles g
1277	269	19.6	389	2	Q7QGN4	Q7qgn4 anopheles g	1350	262	19.1	504	2	Q6PGW7	Q6pgw7 brachydanio
1278	269	19.6	445	2	Q7Q956	Q7q956 anopheles g	1351	261.5	19.0	259	2	Q45048	Q45048 anopheles g
1279	269	19.6	2616	1	NDL_DROME	P98159 drosophila	1352	261.5	19.0	262	2	Q7PX38	Q7px38 anopheles g
1280	268.5	19.5	245	2	Q6DF10	Q6df10 xenopus tro	1353	261.5	19.0	297	2	Q7QNM1	Q7qnm1 anopheles g
1281	268.5	19.5	256	2	Q9Y842	Q9y842 metarhizium	1354	261.5	19.0	324	2	Q6BD08	Q6bd08 drosophila
1282	268.5	19.5	260	2	Q7Z0G4	Q7z0g4 phlebotomus	1355	261.5	19.0	366	2	Q70170	Q70170 mus musculu
1283	268.5	19.5	261	2	Q00344	Q00344 cochliobolu	1356	261.5	19.0	421	1	ACRO_HUMAN	P10323 homo sapien
1284	268.5	19.5	262	1	TRYT_DROER	P54628 drosophila	1357	261.5	19.0	669	2	Q7PWE1	Q7pwe1 anopheles g
1285	268.5	19.5	275	2	Q66UD0	Q66ud0 culicoides	1358	261	19.0	239	2	P97595	P97595 rattus norv
1286	268.5	19.5	707	2	Q70W31	Q70w31 oncorhynchu	1359	261	19.0	246	2	P97611	P97611 rattus norv
1287	268	19.5	182	2	Q6PLJ6	Q6plj6 penaeus jap	1360	261	19.0	262	2	Q7QFW4	Q7qfw4 anopheles g
1288	268	19.5	256	1	PRN3_HUMAN	P24158 homo sapien	1361	261	19.0	316	2	Q9VAQ2	Q9vaq2 drosophila
1289	268	19.5	270	2	Q9VKA9	Q9vka9 drosophila	1362	260.5	19.0	242	1	FIBC_LUMRU	P83298 lumbricus r
1290	268	19.5	277	2	Q6WN60	Q6wn60 brattchiosto	1363	260.5	19.0	242	2	Q96687	Q96687 lumbricus b
1291	267.5	19.5	249	2	Q6IE63	Q6ie63 rattus norv	1364	260.5	19.0	242	2	Q8MX72	Q8mx72 eisenia foe
1292	267.5	19.5	255	2	Q44332	Q44332 manduca sex	1365	260.5	19.0	242	2	Q6T373	Q6t373 eisenia foe
1293	267.5	19.5	280	2	Q6GLK1	Q6glk1 xenopus lae	1366	260.5	19.0	245	2	Q7PFF6	Q7pff6 anopheles g
1294	267	19.4	182	2	Q6PLJ5	Q6plj5 neocaridina	1367	260.5	19.0	264	2	Q9VT25	Q9vt25 drosophila
1295	267	19.4	271	2	Q8SZQ7	Q8szq7 drosophila	1368	260.5	19.0	298	2	Q7PZ90	Q7pz90 anopheles g
1296	267	19.4	388	2	Q8I926	Q8i926 hyphantria	1369	260.5	19.0	688	2	Q9PVI4	Q9pvv4 xenopus lae
1297	267	19.4	222	1	TRYI_DROME	Q9xyy0 drosophila	1370	260	18.9	257	2	Q8I8E2	Q8i8e2 aedes trise
1298	266	19.4	252	2	Q9XYT0	P52905 drosopsais	1371	260	18.9	302	2	Q8I1G9	Q8ilg9 anopheles g
1299	266	19.4	254	2	Q9VEM9	Q9vem9 drosophila	1372	259.5	18.9	252	2	Q6I138	Q6i138 mus musculu
1300	266	19.4	266	2	Q9VEM9	Q9vem9 drosophila	1373	259.5	18.9	275	2	Q66UC8	Q66uc8 culicoides
1301	266	19.4	273	2	Q8MTU7	Q8mtu7 drosophila	1374	259.5	18.9	309	2	Q6DHH4	Q6dhh4 brachydanio
1302	266	19.4	277	2	Q8MLC4	Q8mlc4 drosophila	1375	259.5	18.9	324	2	Q6BD05	Q6bd05 drosophila
1303	266	19.4	400	2	Q9GRG2	Q9grg2 tenebrio mo	1376	259.5	18.9	324	2	Q6BD06	Q6bd06 drosophila
1304	266	19.4	506	2	Q7PR64	Q7pr64 anopheles g	1377	259.5	18.9	324	2	Q6BD16	Q6bd16 drosophila
1305	266	19.4	322	2	Q6BD03	Q6bd03 drosophila	1378	259.5	18.9	511	2	Q9VZH5	Q9vzh5 drosophila
1306	265.5	19.3	434	2	Q9V7S7	Q9v7s7 drosophila	1379	259.5	18.9	546	2	Q8SXG6	Q8sxg6 drosophila
1307	265.5	19.3	444	2	Q9V4W6	Q9v4w6 drosophila	1380	259.5	18.9	248	1	GRAE_MOUSE	P08884 mus musculu
1308	265.5	19.3	251	2	Q9VQ99	Q9vq99 drosophila	1381	259	18.9	263	2	Q9V5X7	Q9v5x7 drosophila
1309	265	19.3	277	2	Q7QKR3	Q7qkr3 anopheles g	1382	259	18.9	279	2	Q7QE41	Q7qe41 anopheles g
1310	265	19.3	322	2	Q98GI6	Q98gi6 rhizobium i	1383	259	18.9	167	2	Q6URK9	Q6urk9 bothrops ja
1311	265	19.3	415	1	ACRO_PIG	P08001 sus scrofa	1384	258.5	18.8	248	2	Q6IE58	Q6ie58 rattus norv
1312	265	19.3	415	2	Q29015	Q29015 sus sp. pre	1385	258.5	18.8	285	2	Q69997	Q69997 streptomyce
1313	265	19.3	247	2	Q7PFF5	Q7pff5 anopheles g	1386	258.5	18.8	459	2	Q9V4W7	Q9v4w7 drosophila
1314	264.5	19.3	248	1	TRYP_FUSOX	P35049 fusarium ox	1387	258.5	18.8	522	2	Q8MQM9	Q8mqm9 drosophila
1315	264.5	19.3	256	1	TRYA_MANSE	P35045 manduca sex	1388	258.5	18.8	1089	2	Q8T3A0	Q8t3a0 ciona intes
1316	264.5	19.3	369	2	VDP_BOMMO	Q07943 bombyx mori	1389	258.5	18.8	267	2	Q9GP27	Q9gp27 drosophila
1317	264.5	19.3	264	1	Q6Q6S3	Q6q6s3 callinectes	1390	258	18.8	269	2	Q7Q5I5	Q7q5i5 anopheles g
1318	264.5	19.3	369	2	Q9PVY2	Q9pvy2 triakis scy	1391	258	18.8	277	2	Q7PG95	Q7pg95 anopheles g
1319	264.5	19.3	719	2	Q15098	Q15098 homo sapien	1392	258	18.8	295	2	O18445	O18445 helicoverpa
1320	264	19.2	176	2	Q96A30	Q96a30 homo sapien	1393	258	18.8	300	2	Q7Q6U0	Q7q6u0 anopheles g
1321	264	19.2	180	2	Q7PXS5	Q7pxg5 anopheles g	1394	258	18.8	352	2	Q7KVM3	Q7kvm3 drosophila
1322	264	19.2	301	2	CAP7_HUMAN	P20160 homo sapien	1395	258	18.8	387	2	Q7RTY4	Q7rty4 homo sapien
1323	263.5	19.2	251	1	Q6RS51	Q6r561 ostrinia nu	1396	258	18.8	196	2	Q6VFC8	Q6vfc8 anopheles g
1324	263.5	19.2	256	2	Q9VMX9	P54630 drosophila	1397	257.5	18.7	248	2	Q6IE09	Q6ie09 rattus norv
1325	263.5	19.2	258	2	Q9VMX9	Q6ick2 homo sapien	1398	257.5	18.7	254	2	Q01136	Q01136 metarhizium
1326	263.5	19.2	281	1	TRYZ_DROER	Q6t775 homo sapien	1399	257.5	18.7	259	2	Q97097	Q97097 anopheles a
1327	263.5	19.2	421	2	Q6ICK2	Q7q5e4 anopheles g	1400	257.5	18.7	254	2	Q97098	Q97098 anopheles a
1328	263	19.1	180	2	Q6T775	Q8ire2 drosophila	1401	257.5	18.7	255	2	Q961Y0	Q961y0 galleria me
1329	263	19.1	241	2	Q7Q5E4	Q9vzt0 drosophila	1402	257.5	18.7	274	2	Q97097	Q97097 anopheles a
1330	263	19.1	248	2	Q8IRE2	Q7qih5 anopheles g	1403	257.5	18.7	259	2	Q6DHC9	Q6dhc9 brachydanio
1331	263	19.1	257	2	Q9VZT0	Q945t9 phytophthor	1404	257.5	18.7	286	2	Q96900	Q96900 scolopendra
1332	263	19.1	272	2	Q7QIH5	Q9n6c6 heliothis z	1405	257.5	18.7	326	2	Q7RTY6	Q7rty6 homo sapien
1333	263	19.1	289	2	Q945T9	Q8in70 drosophila	1406	257	18.7	237	2	Q6LBN2	Q6lbn2 homo sapien
1334	263	19.1	295	2	Q9N6C6	Q8sz60 drosophila	1407	257	18.7	256	2	O18441	O18441 helicoverpa
1335	263	19.1	300	2	Q8IN70	Q6it09 pseudonaja	1408	257	18.7	284	2	Q8MLV8	Q8mlv8 drosophila
1336	263	19.1	405	2	Q8SZ60	P35047 manduca sex	1409	257	18.7	417	2	Q6JE90	Q6je90 homo sapien
1337	263	19.1	467	2	Q6IT09	Q9vrs6 drosophila	1410	256.5	18.7	196	2	Q6VFD0	Q6vfd0 anopheles g
1338	262.5	19.1	256	1	TRYC_MANSE	Q8syb5 drosophila	1411	256.5	18.7	235	1	TRYD_HUMAN	Q9bzj3 homo sapien
1339	262.5	19.1	271	2	Q9VRS6	Q9qwf2 rattus sp.	1412	256.5	18.7	242	2	Q6NTB8	Q6ntb8 homo sapien
1340	262.5	19.1	281	2	Q8SYB5	Q9qwf2 rattus sp.	1413	256.5	18.7	464	2	Q9NK82	Q9nk82 drosophila
1341	262.5	19.1	433	2	Q9QWF2	Q9cvu2 mus musculu	1414	256	18.6	245	2	Q9XY47	Q9xy47 ctenocephal
1342	262.5	19.1	778	2	Q9V519	Q6plj7 fenneropena	1415	256	18.6	265	2	Q9XY55	Q9xy55 ctenocephal
1343	262.5	19.1	108	2	Q9CVU2	Q9vq97 drosophila	1416	256	18.6	267	2	Q9VRU0	Q9vru0 drosophila
1344	262	19.1	183	2	Q6PLJ7		1417	256	18.6	282	2	Q7QCX2	Q7qcx2 anopheles g
1345	262	19.1	245	2	Q9VQ97		1418	256	18.6	403	2	Q9KSQ6	Q9ksq6 vibrio chol



1419	256	18.6	421	2	Q6ZMR5	Q6zmr5	homo sapien
1420	256	18.6	463	2	Q6IT10	Q6it10	pseudonaja
1421	255.5	18.6	220	2	Q6XI43	Q6xi43	drosophila
1422	255.5	18.6	254	2	O18436	O18436	helicopterpa
1423	255.5	18.6	273	2	Q7Z163	Q7z163	dermatophag
1424	255.5	18.6	431	2	Q7PV05	Q7pv05	anopheles g
1425	255	18.6	292	2	Q7PVQ5	Q7pvq5	anopheles g
1426	255	18.6	405	2	Q7PNQ3	Q7pnq3	anopheles g
1427	254.5	18.5	254	2	O18434	O18434	helicopterpa
1428	254.5	18.5	278	2	P91893	P91893	arenicola m
1429	254.5	18.5	357	2	Q7Q092	Q7q092	anopheles g
1430	254.5	18.5	357	2	Q7QKX6	Q7qkx6	anopheles g
1431	254.5	18.5	493	2	Q7PV62	Q7pv62	anopheles g
1432	254.5	18.5	523	2	Q9V819	Q9v819	drosophila
1433	254.5	18.5	524	2	Q8MR00	Q8mr00	drosophila
1434	254.5	18.5	827	2	Q7PZ88	Q7pz88	anopheles g
1435	254	18.5	324	2	Q6BD11	Q6bd11	drosophila
1436	254	18.5	334	2	Q9VEA0	Q9vea0	drosophila
1437	253.5	18.4	282	2	Q64ID4	Q64id4	anthonomus
1438	253	18.4	242	2	Q9XY59	Q9xy59	ctenocephal
1439	253	18.4	251	2	Q9VXC9	Q9vxc9	drosophila
1440	253	18.4	253	2	Q6W741	Q6w741	pediculus h
1441	253	18.4	272	1	SER3 DROME	P17207	drosophila
1442	253	18.4	287	2	Q675S0	Q675s0	oikopleura
1443	252.5	18.4	245	2	Q7Q2Q8	Q7q2q8	anopheles g
1444	252.5	18.4	254	2	Q76954	Q76954	lacanobia o
1445	252.5	18.4	282	2	Q8MJD1	Q8mjd1	canis famil
1446	252.5	18.4	324	2	Q6BD09	Q6bd09	drosophila
1447	252	18.3	235	2	Q7PRK6	Q7prk6	anopheles g
1448	252	18.3	295	2	O18450	O18450	helicopterpa
1449	252	18.3	301	2	Q7Q6T0	Q7q6t0	anopheles g
1450	252	18.3	400	2	Q27081	Q27081	tachypleus
1451	251.5	18.3	186	2	Q6X655	Q6x655	marmota mon
1452	251.5	18.3	266	2	Q8MLC2	Q8mlc2	drosophila
1453	251.5	18.3	267	2	Q9VGB8	Q9vgb8	drosophila
1454	251.5	18.3	276	2	O18443	O18443	helicopterpa
1455	251.5	18.3	318	2	Q7QC37	Q7qc37	anopheles g
1456	251.5	18.3	418	2	Q7Q529	Q7q529	anopheles g
1457	251.5	18.3	520	2	Q8ING0	Q8ing0	drosophila
1458	251	18.3	285	2	Q7Q5K4	Q7q5k4	anopheles g
1459	251	18.3	405	2	Q8MQS8	Q8mq8	apis mellif
1460	250.5	18.2	226	2	Q6XHU4	Q6xhu4	drosophila
1461	250.5	18.2	240	2	Q7PYJ1	Q7pyj1	anopheles g
1462	250.5	18.2	268	2	Q9VT24	Q9vt24	drosophila
1463	250.5	18.2	305	2	Q8MRL2	Q8mrl2	drosophila
1464	250.5	18.2	323	2	Q76920	Q76920	drosophila
1465	250	18.2	124	2	Q8C6G5	Q8c6g5	mus musculu
1466	250	18.2	203	2	Q9NB77	Q9nb77	heliethis z
1467	250	18.2	258	2	Q9VS86	Q9vs86	drosophila
1468	250	18.2	274	2	Q8MUG0	Q8mug0	glossina fu
1469	249.5	18.2	253	2	O18442	O18442	helicopterpa
1470	249.5	18.2	254	2	O18447	O18447	helicopterpa
1471	249.5	18.2	258	2	Q7Q2P0	Q7q2p0	anopheles g
1472	249.5	18.2	269	2	Q7PW15	Q7pw15	anopheles g
1473	249.5	18.2	274	2	Q9VRS7	Q9vrs7	drosophila
1474	249.5	18.2	282	2	O18655	O18655	plodia inte
1475	249.5	18.2	327	2	Q8MS77	Q8ms77	drosophila
1476	249.5	18.2	362	2	Q6LU71	Q6lu71	photobacter
1477	249.5	18.2	520	2	Q8SY93	Q8sy93	drosophila
1478	249	18.1	253	2	Q9NGY5	Q9ngy5	heliethis v
1479	249	18.1	305	2	Q7Q6S4	Q7q6s4	anopheles g
1480	249	18.1	388	2	Q966V2	Q966v2	halocynthia
1481	249	18.1	714	2	Q7PWE5	Q7pwe5	anopheles g
1482	248.5	18.1	296	2	Q9I7I1	Q9i7i1	drosophila
1483	248.5	18.1	381	2	Q8MQY4	Q8mqy4	drosophila
1484	248.5	18.1	746	2	O01654	O01654	halocynthia
1485	248	18.0	141	2	Q6GKZ6	Q6gkz6	drosophila
1486	248	18.0	257	2	Q8IT49	Q8it49	pyrocoelia
1487	248	18.0	257	2	Q945U0	Q945u0	phytophthor
1488	248	18.0	258	2	Q9VZS9	Q9vzs9	drosophila
1489	248	18.0	277	2	Q7QL41	Q7ql41	anopheles g
1490	248	18.0	277	2	Q7QNM2	Q7qnm2	anopheles g
1491	248	18.0	367	2	O70169	O70169	mus musculu

1492	248	18.0	374	2	Q80YD5	Q80yd5	mus musculu
1493	248	18.0	392	2	Q9VMZ3	Q9vmz3	drosophila
1494	248	18.0	401	2	Q6LHI7	Q6lhi7	photobacter
1495	247.5	18.0	260	2	Q9U4I4	Q9u4i4	plodia inte
1496	247.5	18.0	291	2	Q6Y1Y9	Q6y1y9	lygus lineo
1497	247	18.0	243	2	Q7M4I3	Q7m4i3	megabombus
1498	247	18.0	278	2	Q7Q8Q5	Q7q8q5	anopheles g
1499	247	18.0	350	2	Q9VCJ9	Q9vcj9	drosophila
1500	247	18.0	360	2	Q9W1X6	Q9w1x6	drosophila

ALIGNMENTS

RESULT 1

ID	KLKC HUMAN	STANDARD;	PRT;	248 AA.
AC	Q9UKR0; Q9UKR1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)			
DE	(KLK-L5) (UNQ669/PRO1303).			
GN	Name=KLK12; Synonyms=KLKL5;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20118156; PubMed=10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4.";			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;			
RT	"Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5).";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBSJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paepfer B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19ql3 region.";			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wiesand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15057824; DOI=10.1038/nature02399;			
RA	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,			
RA	Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,			
RA	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,			
RA	Caenepeel S., Carrano A.V., Caciile C., Chan Y.M., Christensen M.,			
RA	Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Detter J.C.,			

RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,  
RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,  
RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,  
RA Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,  
RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,  
RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,  
RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,  
RA Rodriguez A., Rogers S., Salamon A., Salazar A., She X., Smith D.,  
RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,  
RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,  
RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,  
RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,  
RA Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9UKR0-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9UKR0-2; Sequence=VSP\_005403;  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein  
CC subfamily.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF135025; AAD26426.2; --  
DR EMBL; AF135025; AAF06065.1; --  
DR EMBL; AF243527; AAG33365.1; --  
DR EMBL; AY358524; AAQ8888.1; --  
DR EMBL; AC011473; AAG23258.1; --  
DR HSSP; P00760; 1EZK.  
DR MEROPS; S01.020; --.  
DR Genew; HGNC:6360; KLK12.  
DR MIM; 605539; --.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 248 Kallikrein 12.  
FT ACT\_SITE 62 62 Charge relay system (By similarity).  
FT ACT\_SITE 108 108 Charge relay system (By similarity).  
FT ACT\_SITE 200 200 Charge relay system (By similarity).  
FT DISULFID 28 161 By similarity.  
FT DISULFID 47 63 By similarity.  
FT DISULFID 133 235 By similarity.  
FT DISULFID 140 206 By similarity.  
FT DISULFID 172 186 By similarity.  
FT DISULFID 196 222 By similarity.  
FT CARBOHYD 24 24 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc. . .) (Potential).  
FT VARSPLIC 236 248 KYVDWIRMIIRNN -> NSTLVGLGTSWNFNQCQPF (in  
FT isoform 2).  
FT /FTId=VSP\_005403.  
SQ SEQUENCE 248 AA; 26733 MW; BB473E98F8BAF703 CRC64;

Query Match 100.0%; Score 1374; DB 1; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.5e-102;  
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60  
Db 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT 60  
QY 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVR 120  
Db 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRPVR 120  
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPGR 180  
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNRPFDLLQCLNLSIVSHATCHGVYPGR 180  
QY 181 TSNMVCAGGVPQDACQGDGGLVCGGVLCGLVSGVPCGQDGIPGVYTYICKYVDW 240  
Db 181 TSNMVCAGGVPQDACQGDGGLVCGGVLCGLVSGVPCGQDGIPGVYTYICKYVDW 240  
QY 241 IRMIMRNN 248  
Db 241 IRMIMRNN 248

RESULT 2  
Q9CV76 PRELIMINARY; PRT; 234 AA.  
ID Q9CV76;  
AC Q9CV76;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
DE library, clone:2310008B01 product:similar to KALLIKREIN 12 (EC  
DE 3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).  
GN Name=KLK12;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]

RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,	
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771(2000).	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,	
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,	
RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,	
RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,	
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,	
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,	
RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,	
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,	
RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,	
RA	Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,	
RA	Muramatsu M., Hayashizaki Y.;	
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
CC	-I- SIMILARITY: Belongs to peptidase family S1.	
DR	EMBL; AK009217; BAB26143.1; -.	
DR	HSSP; P00760; 1EZX.	
DR	MEROPS; S01.020; -.	
DR	MGD; MGI:1916761; Klk12.	
DR	GO; GO:004263; F:chymotrypsin activity; IEA.	
DR	GO; GO:0008233; F:peptidase activity; IEA.	
DR	GO; GO:0004295; F:trypsin activity; IEA.	
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	
DR	InterPro; IPR001254; Peptidase_S1.	
DR	InterPro; IPR001314; Peptidase_S1A.	
DR	InterPro; IPR009003; Pept_Ser_Cys.	
DR	Pfam; PF00089; Trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	SMART; SM00020; Tryp_SPC; 1.	
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KW	Hydrolase; Protease; Serine protease.	
FT	NON_TER 1	
SQ	SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;	
Query Match 69.3%; Score 952.5; DB 2; Length 234;		
Best Local Similarity 70.6%; Pred. No. 1.9e-68;		
Matches 166; Conservative 27; Mismatches 41; Indels 1; Gaps 1;		
Qy	14 LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYVRLG 73	
Db	:                 :       :	
Db	1 LSQADREKIYNGVECVKNSQPWQVGLFHGKYLRCGGVLVDKRWVLTAAHCR-DKYVVRLG 59	
Qy	74 EHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSVQPLPLPND 133	
Db	:       :       :       :       :       :       :	
Qy	60 EHSLTKLDWTEQLRHTTFSITHPSYQGYQNHEHDLRLRLRPILHLTRAVRPVALPSSC 119	
Qy	134 ATAGTECHVSGWGITHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGVPQC 193	
Db	:                 :                 :	
Qy	120 VTTGAMCHVSGWGTNKPDPDFDLRLQCLNLSVTNETCAVFPGRVTENMLCAGSEAGK 179	
Qy	194 DACQDSGGPLVCGGVQLGLVSWGSGPCGDGIPGVYTYICKYVDWIRMIRNN 248	
Db		
Db	180 DACQDSGGPLVCGGVQLGLVSWGSGPCGKGIPGVYTKVCKYTDWIRIVIRNN 234	

RESULT 3  
KLK8\_HUMAN

ID	KLK8_HUMAN	STANDARD;	PRT;	260 AA.
AC	O60259; Q9HCB3; Q9UIL9; Q9UQ47;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Neurosin precursor (EC 3.4.21.-) (NP) (Kalikrein 8) (Ovasin) (Serine			
DE	protease TADG-14) (Tumor-associated differentially expressed gene-14			
DE	protein) (UNQ283/PRO322).			
GN	Name=KLK8; Synonyms=NRPN, PRSS19, TADG14;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hippocampus;			
RX	MEDLINE=98372070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;			
RA	Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;			
RT	"Sequence analysis and expression of human neuropsin cDNA and gene.";			
RL	Gene 213:9-16(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Brain;			
RX	MEDLINE=99203457; PubMed=10102990;			
RA	Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;			
RT	"A novel form of human neuropsin, a brain-related serine protease, is			
RT	generated by alternative splicing and is expressed preferentially in			
RT	human adult brain.";			
RL	Eur. J. Biochem. 260:627-634(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Ovary;			
RX	MEDLINE=99413504; PubMed=10485494;			
RA	Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,			
RA	O'Brien T.J.;			
RT	"Cloning of tumor-associated differentially expressed gene-14, a novel			
RT	serine protease overexpressed by ovarian carcinoma.";			
RL	Cancer Res. 59:4435-4439(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;			
RT	"Molecular cloning and characterization of a novel serine protease,			
RT	ovasin, a potential molecular marker for ovarian carcinomas.";			
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paeper B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P., Gray A.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270(2003).			
RN	[7]			
RP	SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,			









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DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Serine protease; Signal; Zymogen.
FT SIGNAL 1 28
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73
FT ACT_SITE 120 120
FT ACT_SITE 212 212
FT DISULFID 39 173
FT DISULFID 58 74
FT DISULFID 145 246
FT DISULFID 152 218
FT DISULFID 184 198
FT DISULFID 208 233
FT CARBOHYD 110 110
FT STRAND 34 34
FT STRAND 37 38
FT TURN 41 42
FT TURN 45 46
FT STRAND 47 52
FT TURN 53 54
FT STRAND 55 64
FT TURN 65 66
FT STRAND 67 70
FT HELIX 72 74
FT STRAND 80 83
FT STRAND 87 87
FT TURN 88 89
FT STRAND 96 98
FT STRAND 100 105
FT TURN 107 108
FT TURN 114 115
FT TURN 118 119
FT STRAND 122 126
FT STRAND 140 141
FT TURN 148 149
FT STRAND 151 156
FT STRAND 170 170
FT STRAND 172 178
FT HELIX 181 187
FT TURN 189 191
FT TURN 194 195
FT STRAND 196 200
FT TURN 202 203
FT STRAND 206 206
FT TURN 209 210
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FT STRAND 215 218
FT TURN 219 220
FT STRAND 221 228
FT STRAND 235 235
FT TURN 236 237
FT STRAND 238 238
FT STRAND 240 244
FT HELIX 245 256
SQ SEQUENCE 260 AA; 28523 MW; BE5F6F6BE37CD60E CRC64;
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Query Match 45.3%; Score 622.5; DB 1; Length 260;
Best Local Similarity 49.0%; Pred. No. 5.6e-42;
Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

QY 5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWLTAA 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
13 ILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWLTAA 72
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 62 HCSGRYWVRLGEHSLSQLDWTETQIRHSGFSVTHPGYLGAS-TSHEHDLRLRLPVRV 120
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Db 73 HCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSPEDHSHDIMLIRLQNSANL 132
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QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
| : | | | | : | | | | : | | : | | : | | : | | : | | :
Db 133 GDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCEAYPGKI 192
| : | | | | : | | | | : | | : | | : | | : | | : | | :
QY 181 TSNMVCAGVPQDACQDGGPLVCGGVQLGVLWSGSGVPCGQDGIPGVYTYICKYVDW 240
| | | | | : | | | | | : | | | | : | | : | | : | | : | | :
Db 193 TEGMVCAGSSNGADTCQGDSSGGPLVCDGMLQGITWSGS-DPCGKPEKPGVYTKICRYTTW 251
| | | | | : | | | | | : | | | | : | | : | | : | | : | | :
QY 241 IRMIMRN 247
| : | |
Db 252 IKKTMND 258

RESULT 6
NRPN_RAT
ID NRPN RAT STANDARD; PRT; 260 AA.
AC O88780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
DE protease 1).
GN Name=Klk8; Synonyms=Bspl, Nrpn, Prss19;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
RT "Serine proteases in rodent hippocampus.";
RL J. Biol. Chem. 273:23004-23011(1998).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin (By similarity).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
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EMBL; AJ005641; CAA06643.1; -.
DR HSSP; Q61955; INPM.
DR MEROPS; S01.244; -.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
FT SIGNAL 1 28
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73
FT ACT_SITE 120 120
FT ACT_SITE 212 212
FT ACT_SITE 212 212
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FT	DISULFID	39	173	By similarity.
FT	DISULFID	58	74	By similarity.
FT	DISULFID	145	246	By similarity.
FT	DISULFID	152	218	By similarity.
FT	DISULFID	184	198	By similarity.
FT	DISULFID	208	233	By similarity.
FT	CARBOHYD	110	110	N-linked (GlcNAc... ) (Potential).
SQ	SEQUENCE	260 AA;	28510 MW;	58DF4F0602A0B7F5 CRC64;
Query Match				
Best Local Similarity		45.2%;	Score 621.5;	DB 1; Length 260;
Matches 118;		Conservative	32;	Mismatches 90; Indels 3; Gaps 3;
QY	5	IFLLL-CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC	63	
Db	15	LFLMGAWAGLTRAQGSKILEGQECKPHSQPWQTALEQGERLVCGLVGDWRWVLTAAHC	74	
QY	64	SGSRYVVRVRLGEHSLSQLDWTEQIRHSGFSVTHPGVILGAS-TSHEHDLRLRLRLPVRVTS	122	
Db	75	KDKYSVRLGDHSLQKRDEPEQEIQVARSIQHPCFNSNPEDHSHDIMLRLQNSANLGD	134	
QY	123	SVQPLPLPNDCATAGTECHVSGWGITNHPNPFDDLLQCLNLSIVSHATCHGVYPGRITS	182	
Db	135	KVKPIELANLCPKVGQKCIISGWTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITE	194	
QY	183	NMVCAGGVPGQDACQGDSSGPLVCGGVGLQGLVSGVPGCGQDGIPGVYTYICKYVDWIR	242	
Db	195	GMVCAGSSNGADTCQGDSSGPLVCNGVLQGITWGS-DPCGKPEKPGVYTKICRYTNWIK	253	
QY	243	MIM	245	
Db	254	KTM	256	

RESULT 7  
KLKB\_HUMAN STANDARD; PRT; 250 AA.  
AC Q9UBX7; O75837; Q9NS65;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like protease) (UNQ649/PRO1279).  
DE Name=KLK11; Synonyms=PRSS20, TLSP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Hippocampus;  
RX MEDLINE=98438738; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;  
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;  
RT "cDNA cloning and expression of a novel serine protease, TLSP.";  
RL Biochim. Biophys. Acta 1399:225-228(1998).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Hippocampus, and Prostate;  
RX MEDLINE=20329229; PubMed=10872828; DOI=10.1006/bbrc.2000.2761;  
RA Mitsui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;  
RT "A novel isoform of a kallikrein-like protease, TLSP/hippostasin, (PRSS20), is expressed in the human brain and prostate.";  
RL Biochem. Biophys. Res. Commun. 272:205-211(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;  
RA Yousef G.M., Scorilas A., Diamandis E.P.;  
RT "Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family.";  
RL Genomics 63:88-96(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1).

RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.;  
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiewand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX PubMed=15057824; DOI=10.1038/nature02399;  
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E., Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C., Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J., Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E., Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M., Rubin E.M., Lucas S.M.;  
RT "The DNA sequence and biology of human chromosome 19.";  
RL Nature 428:529-535(2004).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Possible multifunctional protease. Efficiently cleaves bz-Phe-Arg-4-methylcoumaryl-7-amide, a kallikrein substrate, and weakly cleaves other substrates for kallikrein and trypsin.  
CC -!- SUBCELLULAR LOCATION: Secreted.



```
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UBX7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UBX7-2; Sequence=VSP_005402;
CC -!- TISSUE SPECIFICITY; Expressed in brain, skin and prostate. Isoform
CC 1 is expressed preferentially in brain; isoform 2 in prostate.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -----
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CC -----
CC EMBL; AB012917; BAA33404.1; ALT_INIT.
CC EMBL; AB013730; BAA88713.1; -.
CC EMBL; AB041036; BAA96797.1; -.
CC EMBL; AF164623; AAD47815.1; -.
CC EMBL; AF243527; AAG33364.1; -.
CC EMBL; AY359014; AAO89373.1; -.
CC EMBL; AC011473; AAG23257.1; -.
CC EMBL; BC022068; AAG22068.1; -.
CC HSSP; P00760; 1EXZ.
CC MEROPS; S01.257; -.
CC Genew; HGNC:6359; KLK11.
CC H-InvDB; HIX0015375; -.
CC MIM; 604434; -.
CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
CC InterPro; IPR009003; Pept_Ser_Cys.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; Zymogen.
FT SIGNAL 1 18 Potential.
FT PROPEP 19 21 Activation peptide (Potential).
FT CHAIN 22 250 Kallikrein 11.
FT ACT_SITE 62 62 Charge relay system (By similarity).
FT ACT_SITE 110 110 Charge relay system (By similarity).
FT ACT_SITE 203 203 Charge relay system (By similarity).
FT DISULFID 28 163 By similarity.
FT DISULFID 47 63 By similarity.
FT DISULFID 135 237 By similarity.
FT DISULFID 142 209 By similarity.
FT DISULFID 174 188 By similarity.
FT DISULFID 199 224 By similarity.
FT CARBOHYD 99 99 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 165 165 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 181 181 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 210 210 N-linked (GlcNAc . .) (Potential).
FT VARSPLIC 1 1 M -> MQLRLWLRDWKSSGRGLTAAKEPGARSSPLQAM
FT (in isoform 2).
FT FTId=VSP_005402.
FT SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;

Query Match 45.0%; Score 618.5; DB 1; Length 250;
Best Local Similarity 48.2%; Pred. No. 1.1e-41;
Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

QY 3 LSIFLLLCVLGSLQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH 62
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 4 LQILLALATGLVGGET-RIKGFCEKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH 62
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 63 CSGSRYWVRLGEHSLQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLRLPVRV 120
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Db 63 CLKPRYIVHLGQHNLCQKEGCEQTRTATESFPHPGFNNSLPNKHNDIMLVKMASPVSI 122
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHRPNFPDLLQCLNLSIVSHATCHGVYPGRI 180
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 123 TWAVRPLTLSSRCVTAGTSLISGWGSTSSPQLRPLHTLRCAITIIIEHQKCNAYPGNI 182
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 181 TSNMVCAG-GVPGQDACOGDSGGPLVCGGVLGQLVSGSVGPGCGDGIPIGVYTIKCYVD 239
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 183 TDTMVCASVQEGGKDCQDSGGPLVCNQSLOQIIISWGQ-DPCAITRKPGVYTKVCKYVD 241
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 240 WIRMIMRNN 248
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 242 WIQETMKN 250
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :

RESULT 8
Q7JIG6 PRELIMINARY; PRT; 255 AA.
AC Q7JIG6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KKK15.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080;
RA Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.;
RT "Glandular kallikreins of the cotton-top tamarin: molecular cloning of
RT the gene encoding the tissue kallikrein.";
RL DNA Cell Biol. 19:721-727(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Olsson Y., Persson M., Lundwall A.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AF173845; AAS45302.1; -.
DR HSSP; P00761; IAKS.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 28078 MW; A040914ABC8FEC8D CRC64;

Query Match 44.5%; Score 611; DB 2; Length 255;
Best Local Similarity 49.4%; Pred. No. 4.6e-41;
Matches 118; Conservative 31; Mismatches 76; Indels 14; Gaps 5;

QY 21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGRYWVRLGEHSLSQL 80
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 20 KLEGEECAPHSQPWQVQALYERGRFNCGLASLISPHWVLSAAHCSGRFMRVRLGEHNLKR 79
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 81 DWTEQIRHSGFSVTHPGYLCASTSHEHDLRLRLPVRVTSSVQPLPLPNDCATAGTEC 140
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 80 DGPEQLRTASRVIPHPRY--EASRRHDIIMLRVQPARLTPQVRPVVLPTRCPHPGEAC 137
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
QY 141 HVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATCHGVYPGRIITSNMVCAGGV 190
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
Db 138 VVSGWGLVSHNEPGTTGRPQSQVSLPDTLHCANISIIISDASCDKNYPGRLLTNTMVCAGAE 197
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
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RT "Molecular cloning of the human kallikrein 15 gene (KLK15). Up-regulation in prostate cancer.";  
RT J. Biol. Chem. 276:53-61(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;  
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepers B., Wang K.;  
RA "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";  
RT cluster located in chromosome 19q13 region.";  
RL Gene 257:119-130(2000).  
RN [3]  
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;  
RA Dihanich M.E., Spiess M.;  
RT "A novel serine proteinase-like sequence from human brain.";  
RL Biochim. Biophys. Acta 1218:225-228(1994).  
RN [4]  
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).  
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;  
RA Hillman R.T., Green R.E., Brenner S.E.;  
RT "An unappreciated role for RNA surveillance.";  
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).  
CC -!- FUNCTION: Protease whose physiological substrate is not yet known.  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q9H2R5-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9H2R5-2; Sequence=VSP\_005405;  
CC Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;  
CC Name=3;  
CC IsoId=Q9H2R5-3; Sequence=VSP\_005406, VSP\_005407;  
CC Name=4;  
CC IsoId=Q9H2R5-4; Sequence=VSP\_005404;  
CC TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon testis and kidney.  
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.  
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DR EMBL; AF242195; AAG09469.1; -.  
DR EMBL; AF242195; AAG09470.1; -.  
DR EMBL; AF242195; AAG09471.1; -.  
DR EMBL; AF242195; AAG09472.1; -.  
DR EMBL; AF243527; AAG33354.1; -.  
DR EMBL; X75363; CAA53145.1; ALT\_SEQ.  
DR HSSP; P00760; 1EZK.  
DR MEROPS; S01.081; -.  
DR Genew; HGNC:20453; KLK15.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00020; Tryp\_SPC; 1.  
DR PROSITE; PS0240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS0134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; FALSE\_NEG.

KW Alternative splicing; Glycoprotein; Hydrolase; Serine protease;  
KW Signal; Zymogen.  
FT SIGNAL 1 16 Potential.  
FT PROPEP 17 21 Activation peptide (Potential).  
FT CHAIN 22 256 Kallikrein 15.  
FT ACT\_SITE 62 62 Charge relay system (By similarity).  
FT ACT\_SITE 106 106 Charge relay system (By similarity).  
FT ACT\_SITE 209 209 Charge relay system (By similarity).  
FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 232 232 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 122 206 Missing (in isoform 4).  
FT VARSPLIC 122 256 Missing (in isoform 2).  
FT VARSPLIC 161 161 /FTId=VSP\_005405.  
FT VARSPLIC 162 256 V -> G (in isoform 3).  
FT VARSPLIC 162 256 /FTId=VSP\_005406.  
FT VARSPLIC 162 256 Missing (in isoform 3).  
FT CONFLICT 147 160 SHNEPGTAGSPRSQ -> PLSSP (in Ref. 2).  
FT SEQUENCE 256 AA; 28087 MW; B5EBF8D6022786B5 CRC64;  
SQ  
Query Match 43.6%; Score 599; DB 1; Length 256;  
Best Local Similarity 47.1%; Pred. No. 4.2e-40;  
Matches 121; Conservative 32; Mismatches 88; Indels 16; Gaps 6;  
QY 5 IFLLLCVLGLSQAAT--PKIFNGTECGRNSQPWQVQLFEGTSLRCGGVLIDHRWVLTAAH 62  
Db 3 LLLTSLFLLASTAAQDGDKLLEGDECAHPHQWQVQVLYERGRFCGASLISPHWVLSAAH 62  
QY 63 CSGSRYVWRLGEHSLQDWTETQIRHSGFVTHPGVLCAGSTSHEDLRLRLPVRVTS 122  
Db 63 CQSRFMRVRLGEHNLKRDGPEQLRTTSRVIPHPRY--EARSHRNDIMLLRLVQPARLNP 120  
QY 123 SVQPLPLPNDCATAGTECHVSGWGITNH-----PRN--PFDDLQCLNLSIVSHATC 172  
Db 121 QVRPAVLPTRCPPHGEACVVGWGLVSHNEPGTAGSPRSQVSLPDTLHCANISIIISDTSC 180  
QY 173 HGVPYGRITSNMVCAGGV-PGQDACQGDGSGPLVCGVLCGLVSGVSGPCGQDGIPGVY 231  
Db 181 DKSYPGRLTNTWVCAGAEGRGAESCEGDSGGPLVCGGILQGVISWGDV-PCDNTTKPGVY 239  
QY 232 TYICKYVDWIRMIRNN 248  
Db 240 TKVCHYLEWIRETKRN 256  
RESULT 14  
Q9QYN4  
ID Q9QYN4 PRELIMINARY; PRT; 249 AA.  
AC Q9QYN4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hippostasin.  
GN Name=2310015I08Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;  
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;  
RT "cDNA cloning and tissue-specific splicing variants of mouse hippocasin/TLSP (PRSS20).";  
RL Biochim. Biophys. Acta 1494:206-210(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Yamaguchi N., Mitsui S.;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to peptidase family S1.



DR	EMBL; AB016226; BAA88825.1; -.	
DR	HSSP; P00760; 1EZX.	
DR	MEROPS; S01.257; -.	
DR	MGD; MGI:1929977; 2310015I08Rik.	
DR	GO; GO:0005615; C:extracellular space; TAS.	
DR	InterPro; IPR001254; Peptidase_S1.	
DR	InterPro; IPR001314; Peptidase_S1A.	
DR	InterPro; IPR009003; Pept_Ser_Cys.	
DR	Pfam; PF00089; Trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	SMART; SM00020; Tryp_SPC; 1.	
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
KW	Hydrolase; Protease; Serine protease.	
SQ	SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;	
Query Match 43.5%; Score 597.5; DB 2; Length 249;		
Best Local Similarity 47.0%; Pred. No. 5.4e-40;		
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;		
QY	1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT	60
Db	1 MILRLIALALVTGHVGET-RIIKGYECPHSPQWQVALFQKTRLLCGATLIAPKWLTA	59
QY	61 AHCSGRYWRVLGEHLSQLDWTETQIRHSGFSVTHPGYLGA--STSHEHDLRLRLP	118
Db	60 AHCRKPHYVILLGEHNLEKTDGCEQRRMATESFPHPDFNNSLPNKDHRNDIMLVK	119
QY	119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPNPFPPDLLQCLNLSIVSHATCHGV	178
Db	120 FFTRAVQPLTLPSPHCVAAGTSLISGWGTTSSPQLRLPHSLRCANVSIIEHKECK	179
QY	179 RITSNMVCAG-GVPGQDACQSGGGLVCGGLVQLGVSWSVGPCGDGIPGVYTVICKY	237
Db	180 NITDTMLCASVRKEGKDSQCGSGGLVLCNGSLQGIISWGQ-DPCA	238
QY	238 VDWIRIMMRNN 248	
Db	239 FNNIHEVMRNN 249	
RESULT 15		
Q9QYN3	PRELIMINARY; PRT; 276 AA.	
ID	Q9QYN3	
AC	Q9QYN3;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN	
DE	full-length enriched library, clone:2310015I08 product:protease,	
DE	serine, 20, full insert sequence) (Mus musculus adult male tongue	
DE	cDNA, RIKEN full-length enriched library, clone:2310040F07	
DE	product:protease, serine, 20, full insert sequence).	
GN	Name=2310015I08Rik;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Prostate;	
RX	MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;	
RA	Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;	
RT	"cDNA cloning and tissue-specific splicing variants of mouse	
RT	hippostasin/TLSP (PRSS20).";	
RL	Biochim. Biophys. Acta 1494:206-210(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Prostate;	
RX	MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;	
RA	Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;	
RT	"cDNA cloning and tissue-specific splicing variants of mouse	
RT	hippostasin/TLSP (PRSS20).";	
RL	Biochim. Biophys. Acta 1494:206-210(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Prostate;	
RA	Yamaguchi N., Mitsui S.;	
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	
RN	[3]	

RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	
RA	Carninci P., Hayashizaki Y.;	
RT	"High-efficiency full-length cDNA cloning.";	
RL	Meth. Enzymol. 303:19-44(1999).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RX	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	
RA	RIKEN FANTOM Consortium;	
RT	"Functional annotation of a full-length mouse cDNA collection.";	
RL	Nature 409:685-690(2001).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RA	The FANTOM Consortium,	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;	
RT	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs.";	
RL	Nature 420:563-573(2002).	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;	
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to	
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";	
RL	Genome Res. 10:1617-1630(2000).	
RN	[7]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;	
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	
RA	Konno H., Akiyama J., Nishi K., Kitsu nai T., Tashiro H., Itoh M.,	
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,	
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,	
RA	Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,	
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format	
RT	sequencing pipeline with 384 multicapillary sequencer.";	
RL	Genome Res. 10:1757-1771(2000).	
RN	[8]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Tongue;	
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,	
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,	
RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,	
RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,	
RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,	
RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,	
RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,	
RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,	
RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,	
RA	Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,	
RA	Muramatsu M., Hayashizaki Y.;	
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
CC	-I- SIMILARITY: Belongs to peptidase family S1.	
DR	EMBL; AB016227; BAA36955.1; -.	
DR	EMBL; AK009360; BAB26241.2; -.	
DR	EMBL; AK009720; BAB26461.2; -.	
DR	HSSP; P00760; 1EZX.	
DR	MEROPS; S01.257; -.	
DR	MGD; MGI:1929977; 2310015I08Rik.	
DR	GO; GO:0005615; C:extracellular space; TAS.	
DR	InterPro; IPR001254; Peptidase_S1.	
DR	InterPro; IPR001314; Peptidase_S1A.	
DR	InterPro; IPR009003; Pept_Ser_Cys.	
DR	Pfam; PF00089; Trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	SMART; SM00020; Tryp_SPC; 1.	



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